

## FIGURE 1

ID-65

Clone 3-60

5  
GTGTTTATGATGAAAAAAGGACAAGTAAATGATACTAAGCAA  
TCTTACTCTCTACGTAAATATAAATTTGGTTTAGCATCAGTAA  
TTTTAGGGTCATTCATAATGGTCACAAGTCCTGTTTTTGCGGA  
TCAAACCTACATCGGTTCAAGTTAATAATCAGACAGGCACTAG  
10 TGTGGATGCTAATAATTCTTCCAATGAGACAAGTGCGTCAAGT  
GTGATTACTTCCAATAATGATAGTGTTCAAGCGTCTGATAAAG  
TTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTC  
CTTTAGTAGAGACAAAGCCAATGGTGGAAAAAACATTACCTG  
AACAAGGGAATTATGTTTATAGCAAAGAAACCGAGGTGAAAA  
15 ATACACCTTCAAAATCAGCCCCAGTAGCTTTCTATGCAAAGAA  
AGGTGATAAAGTTTTCTATGACCAAGTATTTAATAAAGATAAT  
GTGAAATGGATTTTCATATAAGTCTTTTGGTGGCGTACGTCGAT  
ACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTTCAGAGA  
CTAAAGCACCTACTCCTGTAACAAATTCAGGAAGCAATAATC  
20 AAGAGAAAATAGCAACGCAAGGAAATTATACATTTTTCACATA  
AAGTAGAAGTAAAAAATGAAGCTAAGGTAGCGAGTCCAATC  
AATTTACATTGGACAAAGGAGACAGAATTTTTTACGACCAA  
TACTAACTATTGAAGGAAATCAGTGGTTATCTTATAAATCATT  
CAATGGTGTTTCGTCGTTTTGTTTTGCTAGGTAAAGCATCTTCA  
25 GTAGAAAAAACTGAAGATAAAGAAAAAGTGTCTCCTCAACCA  
CAAGCCCGTATTACTAAAACCTGGTAGACTGACTATTTCTAACG  
AAACAACCTACAGGTTTTGATATTTTAATTACGAATATTAAAGA  
TGATAACGGTATCGCTGCTGTTAAGGTACCGGTTTGGACTGAA  
CAAGGAGGGCAAGATGATATTAATGGTATACAGCTGTAACCT  
30 ACTGGGGATGGCAACTACAAAGTAGCTGTATCATTTGCTGAC  
CATAAGAATGAGAAGGGTCTTTATAATATTCATTTATACTACC  
AAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACTAAAG  
TGACAGTAGCTGGAACCTAATTCTTCTCAAGAACCTATTGAAAA  
TGGTTTACCAAAGACTGGTGTTTATAATATTATCGGAAGTACT  
35 GAAGTAAAAAATGAAGCTAAAATATCAAGTCAGACCCAATTT  
ACTTTAGAAAAAGGTGACAAAATAAATTATGATCAAGTATTG  
ACAGCAGATGGTTACCAGTGGATTTCTTACAAATCTTATAGTG  
GTGTTTCGTCGCTATATTCCTGTGAAAAAGCTAACTACAAGTAG  
TGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCC  
40 CAACTTACCTAAACAGGTACCTATACATTTACTAAAACCTGTA  
GATGTGAAAAGTCAACCTAAAGTATCAAGTCCAGTGGAATTT  
AATTTTCAAAGGGTGAAAAAATACATTATGATCAAGTGTTA  
GTAGTAGATGGTCATCAGTGGATTTTCATACAAGAGTTATTCCG  
GTATTCGTCGCTATATTGAAATTTAA

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A) Length: 1642 bp - 547 aa (full length gene)

Potential leader peptide sequence

ID-66

ATGATATTGAGACGTGCAACTATTGTTTTATGGCAACTGGGTATCGCCATT  
TCTCTCATTCTTAGTATTCTAGCCTTAAATCTTTATTTCCATAGTACTCCCTT  
30 GCAAACCAATGCAGCTTTACGGAACCTTGCTCCTTCATTAAACCATCTTTTT  
GGGACAGATGGTTTAGGTAGGGATATGTTTGTGAGAACGATTAAAGGACT  
TTATTTCTCTCTACAAGTCGGCTTATTAGGTGCCCTTATGGGGGTCATTCTG  
GCGACAGTTTTTTGGAGTGCTTGCAGGTTTAGGAAATAGCATTATTGATAAA  
ATAATAGCATGGTTAGTTGATTTGTTTATTGGTATGCCTCATTGATTTTTA  
35 TGATTCTCATTTCTTTTGTTGTTGGGAAAGGTGCTCAAGGGGTCATCATTGC  
AACGGCTGTTACACATTGGCCTTCTTTAGCAAGGCTTATCCGCAATGAAGT  
CTATCATCTAAAGAATAAAGAATTTGTCCAACCTTCTAAAAGTATGGGAAA  
AACGCCTTATTATATTGTGAGGCATCATATCCTGCCTTTGATTGCTTCTCAA  
ATTTTCATTGGTTTTATCCTCTTATTTCCACATGTCATCCTACATGAAGCAT  
40 CAATGACTTTCTTAGGATTTGGGCTCTCTGCCGAACAACCTTCGGTTGGTA  
TCATTCTGTGAGAGGCAGCTAAGCATATCTCTCTTGGAATTTGGTGGTTGG  
TTATCTTTCCAGGACTTTATCTTATTTTGGTTGTCAATGCATTTGATACTAT  
CGGAGAATCTTTAAAGAACTCTTTTACCCTCAAACCTGATCATTTTTTAG

MILRRRTIVLWQLGIAISLILSILALNLYFHSTPLQTNAALRNLAAPSLNHLFGTD  
GLGRDMFVRTIKGLYFSLQVGLLGALMGVILATVFGVLAGLGNSIIDKIIAWL  
VDLFIGMPHLIFMILISFVVGKGAQGVIIATAVTHWPSLARLIRNEVYHLKNKE  
5 FVQLSKSMGKTPYYIVRHHILPLIASQIFIGFILLFPHVILHEASMTFLGFGLSAE  
QPSVGIILSEAAKHISLGNWWLVIFPGLYLILVVNAFDTIGESLKKLFPQTDHF  
\*

10 Sequence description

A) Length: 822 bp - 274 aa (full length gene)

B) Sequence Characteristics:

Potential leader peptide sequence

15 Orf is preceded by a potential Shine-  
Dalgarno sequence.

ID-78

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Clone 3-5b

ATGACAGAAACATTATTAAGCATTAAAGACCTCTCCATCACCTTCACTCAA  
TACGGAAGATTTTTAAAACCATTTCAATCAACACCGATACAAGCGCTGA  
25 ATTTAGAAATTA AAAAAGGTGAGTTATTAGCTATTATAGGTGCTAGTGGTT  
CGGGGAAGAGTTTATTAGCACATGCTATTATGGATATTCTTCCTAAAAATG  
CATCTGTAACAGGAGATATGATTTATCGTGGTCAATCACTAAATTCTAAAC  
GCATTAAACAGTTGCGAGGAAAAGATATTACGTTGATTCCACAATCAGTTA  
ATTATTTAGATCCATCTATGAAAGTCAAACATCAGGTGCGCTTAGGTATCT  
30 CAGAAAATTCAAAGGCTACTCAAGAAGGATTGTTTCAACAGTTTGGTTTAA  
AAGAAAGTGATGGTGACTTGGATCCTTTCCAACCTTTCTGGCGGAATGCTCC  
GACGTGTTTTGTTTACAACGTGTATTAGTGATAAGGTTTCTTTGATTATTGC  
GGATGAGCCCACCCCTGGATTACATCCAGATGCTCTGCAAATGGTTTTAGA  
CCAACACTACGCTCCTTTGCAGATAAAGGAATAAGCGTTATATTTATCACTCA  
35 TGATATTGTAGCAGCTAGTCAAATTGCTGATCGTATTACTATTTTTAAAGA  
GGGAAAAGCTATTGAAACAGCTCCAGCTAGTTTCTTTAGCGGAAATGGAG  
AGCAGTTACAAACAGAATTTGCTAGAAGTTTATGGCGCTCTCTCCACAGC  
AAGAATTTTTGAAAGGAGTTACTCATGACCTTAGAGGCTAA

40

MTETLLSIKDLSITFTQYGRFLKPFQSTPIQALNLEIKKGELLAHIGASGSGKSLL  
AHAIMDILPKNASVTGDMIYRGQSLNSKRIKQLRGKDITLIPQSVNYLDPSMK  
VKHQVRLGISENSKATQEGLFQQFGLKESDGDLDPFQLSGGMLRRVLFTTCIS  
DKVSLIIADEPTPGLHPDALQMVLQDLRSFADKGISVIFITHDIVAASQIADRITI  
FKEGKA IETAPASFFSGNGEQLQTEFARSLWRSLPQQEFLKGVTHDLRG\*

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## 40

This gene was not isolated using the LEEP system. However in determining a full length gene sequence for ID-76, this gene was identified upstream.

ID-80

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Clone 2-17

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TTGCGGACAATTACGTTCAAACACAATGAAACGCGATCGTCAAAAAGCGA  
AGGTAGGGCGGTAATGCTTAAAAGATTATTTACTGAAGATGGGGAATTGA  
CAAAGATTAGTCGTCGTTTCGTTTGGATGTTAGTGGTTATCTATTGTCTTAT  
TATTGTCAGGATGTGTTTTGGGCCTCAAATTATGATTGAGGGGGTATCAAC  
TCCGAATGTTTCAGCGCTTCGGAAGAATTGTAGCTCTTTTAGTACCATTAA  
TTCTTTTCGTAGTTTAGATCAGCTAACTAGCTTTAAAGAGATTTTTTGGGTT  
ATTGGTCAAAAATGTAGTGAATATTTTACTGCTGTTTCCTCTCATTATAGGGT  
TACTATCCCTAAAGCCAAGTTTACGGAAATATAAAAAGCGTTATATTACTTG  
CTTTCTTGATGTCTCTTTTCATAGAGTGTACTCAAGTTGTTTTAGATATTTT  
AATAGATGCTAATCGGGTTTTTGAATCGACGATCTATGGACAAATACCTT  
AGGCGGTCCTTTTCGCCCTATGGAGTTATCGAAACATAAAAGGTTGGCTTCT  
AACTATTAGAAAATGA

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MRTITFKHNETRSSKSEGRAVMLKRLFTEDGELTKISRRFVWMLVVIYCLIIVR  
MCFGPQIMIEGVSTPNVQRFGRIVALLVPFNSFRSLDQLTSFKEIFWVIGQNVV  
NILLFPLIIGLLSLKPSLRKYKSVILLAFLMSLFIECTQVVLIDILIDANRVFEIDD  
LWTNTLGGPFALWSYRNIKGWLLTIRK\*

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Sequence description

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A) Length: 579 bp - 193 aa (full length gene)

B) Sequence Characteristics:

Possesses a potential leader peptide sequence

No obvious Shine-Dalgarno, but the 'TTG' codon  
may not be the actual translation start point.

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A methionine (ATG) that occurs ~22 codons  
downstream of the 'TTG' is preceded by a  
potential Shine-Dalgarno sequence and may  
represent the actual start codon.

ID 81

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Clone 3-1

TTGAAAAATTTAAATCGTTATGTAGTTGCGGTTTCTGGAGTCGTTTTACATT  
 TAATGCTAGGATCAACTTATGCTTGGAGTGTGTTTCGTAACCCAATTATCT  
 CAGAGACTGGTTGGGATATTTTCATCAGTTTCATTCGCTTTTGTGCTAT  
 TTTTGTCTAGGAATGTCTGCAGCTTTTATGGGACACTTAGTAGAGCGTTTT  
 5 GGCCTAGGATAATGGGAATGATTTCTGCTATTTTATATGGAGCAGGGAAT  
 GTGTTAACAGGCTTAGCCATTGAACTCAGCAGTTATGGTTACTGTATGTT  
 GCATACGGTATTTTAGGAGGAATCGGACTTGGTTCAGGTTATATTACTCCA  
 GTATCGACTATTATTAAATGGTTTCCTGATAGGAGGGGACTAGCAACAGG  
 ATTCGCTATTATGGGATTTGGCTTTGCTTCTTTAGTAACAAGTCCGCTTGCA  
 10 CAATCCTTACTGATTAGGATTGGTGTGGGTAAAACGTTTTATATTTTGGGA  
 TTAGTATATTTTTTTGTTCATGATGATTGCCTCACAATTTATTAAACAACCAC  
 CTCAGGAAAAAATAACTATTTTGACTCACGATGGTAAAAAGAATGCTATG  
 AATTCACAAATTATCACTGGATTAAAAGCAAACGTCGCTATAAAATCAAA  
 AACCTTTTACATCATTGTTGACCTTGTTTATTAATATTCGTGTGGCTTA  
 15 GGTTTAATATCAGCAGCTTCACCAATGGCACAAGATTTAGCAGGCTATTCC  
 GCAGAATCTGCAGCCTTATTAGTAGGGGTACTAGGGATATTTAACGGTTTT  
 GGACGTCTGTTATGGGCAAGTCTCTCTGACTACATTGGACGCCCGTTGACC  
 TTTATAATATTATTTATTGTGAACCTTATTATGACTTCTAGTTTATTTTTGTC  
 ATTCAATGCTATTGTATTTGCAATAGCGATGTCTATTTTAATGACTTGTTAT  
 20 GGTGCAGGTTTTTCCTTATTACCTGCTTATCTAAGTGATATTTTTGGAACAA  
 AGGAATTAGCTACTTTACATGGTTATAGTTTAACAGCATGGGCAATAGCAG  
 GTCTGTTTGGGCCCTATTGTTATCAAAGACATATTCATGGGGAAATTCCT  
 ATCAATTGACATTAATGGTTTTTGGTTTTTTATTCTTATTCGGATTATTGTTA  
 25 TCTCTATATTTAAGAAAATTAACAATAAAGTTGTGTAG  
  
 LKNLNRYVVAVSGVVLHMLGSTYAWSVFRNPIISETGWDISSVSFAFSLAIFC  
 LGMSAAFMGHLVERFGPRIMGMISAILYGAGNVLTGLAIETQQLWLLYVAYG  
 ILGGIGLGSYITPVSTIIKWFPDRRGLATGFAIMGFGFASLVTSPLAQSLIRIG  
 30 VGKTFYILGLVYFFVMMIASQFIKQPPQEKITILTHDGKKNAMNSQIITGLKAN  
 VAIKSKTFYIIWLTLFINISGLGLISAASPM AQDLAGYSAESAALLVGVLGIFN  
 GFGRLLWASLSDYIGRPLTFILFIVNFIMTSSLFLSFNAIVFAIAMSILMTCYGA  
 GFSLLPAYLSDIFGTELATLHGYSLTAWAIAAGLFGPLLLSKTYSWGN SYQLTL  
 MVFGFLFLFGLLLSLYLRKLTTKVV\*

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Sequence description:

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A] Length 1221 bp - 407 a.a (full length gene).

B] TTG start codon with Shine-Dalgarno sequence upstream. Obvious signal peptide, with hydropathy plot exhibiting many possible membrane spanning regions, indicating protein to be transmembrane.

5 ID-82

Clone 48

10 ATGGCAGATAAAAAACAGAACATTTAAACTTGTAGGTGCAGGATCTTCTAG  
CACACAAGAAAAAATTGAAAAGCCTGCTCTTTTCGTTTATGCAAGATGCGTG  
GCGTCGCTTGAAAAAAAACAAATTAGCAGTAGTTTCACTCTATTTATTAGC  
TCTTTTACTTACTTTTTTCGTTAGCCTCAAATTTATTTGTAAGTCAAGGAT  
15 GCTAATGGGTTTGATTTCGAAAAAAGTAACGACATATCGCAACTTACCACCT  
AAATTGAGTTCAAACCTTCCTTTTTTGAATGGTAGCATTAATCCATCA

MADKNRTFKLVGAGSSSTQEKIEKPALSFMQDAWRRLKKNKLAVVSLYLLA  
LLLTFSLASNLFVTQKDANGFDSKKVTTYRNLPPKLSSNLPFWNGSINPS

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Sequence description:

A] Current length is 303 bp - 101 aa  
B] No obvious signal peptide but Shine  
25 Dalgarno sequence upstream of the ATG start  
codon. Not identified directly using the LEEP system but was found  
directly downstream of ID-34 described in WO 00/06736.

30 ID-83

Clone 98

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ATGAAAATAGTAGTACCAGTAATGCCTCGCAGTCTTGAAGAGGCTCAAGA  
AATAGATTTATCAAAATTTGATAGTGTTGATATTATTGAATGGCGAGCTGA  
TGCCTTACCAAAGGATGACATTATTAATGTAGCTCCAGCTATTTTTGAGAA  
ATTCGCAGGTCATGAAATTATTTTTACTTTTCGTACAACGCGTGAAGGTGG  
40 TAATATTGTCTTATCTGATGCTGAGTATGTTGAGTTAATCCAGAAAATTAA  
TTCTATCTACAATCCAGATTATATTGATTTTGAGTATTTTTCACATAAAGAA  
GTTTTTCAAGAAATGCTAGAATTTCCAAATTTAGTCCTGTCTTATCACAATT  
TTCAAGAGACACCGGAGAATATTATGGAGATATTTTCAGAAATTAACAGCC  
CTAGCACCACGAGTTGTGAAAATCGCAGTAATGCCAAAGAATGAACAAGA

5 TGTCTTAGACGTTATGAATTACACTCGCGGTTTCAAGACTATTAATCCTGA  
TCAAGTTTATGCGACGGTATCTATGAGTAAAATTGGACGTATTTCTCGTTTT  
GCTGGTGATGTAACCTGGATCTAGTTGGACATTTCATATTTAGATTCATCT  
ATCGCACCCGGACAAATTACTATTTTCAGAGATGAAGCGTGTCAAAGCATT  
GCTTGACGCTGACTGA

10 MKIVVPVMPRSLEEAEIDLSKFDSVDIIEWRADALPKDDIINVAPAI FEKFAG  
HEIIFTFRTTREGGNIVLSDAEYVELIQKINSIYNPDYIDFEYFSHKEVFQEMLEF  
PNLVLSYHNFQETPENIMEIFSELTALAPRVVKIAVMPKNEQDVLDMNYTRG  
FKTINPDQVYATVSMISKIGRISRFAGDVTGSSWTFAYLDSSIAPGQITISEMKRV  
KALLDAD\*

15 Sequence description:

A] Length 678 bp, 225 aa (full length gene)  
B] No obvious signal peptide, but there is a  
Shine Dalgarno immediately upstream of ORF.

20 ID-84

25 Clone RS-52

30 ATGAAAGACTTATTTGCAACAACAGAAGCATCATCAAGGAAACAGGAACA  
AGATAGAATTGTCAATTACATAAAACAACATGTTGAGTTAACAAATGGTA  
ATCAAATAAAAAAAATTGAGTTTATCGACTTTCAAAAAAATGAGATGACA  
GGTACATGGGGAATTTCTACTAAAATTAATGAACAATTTTCGATTAGTTTT  
TCTGAAGATAGAATTGGTGGTAAACTTAGAGCATTAGGATATCAACCGAA  
TGAAATAGGTTTTTCAAAGGACATCAATAGTAATAATCAAATGTTAATGA  
TATTGAAGTGATTTATATGAAGAAAGAATAG

35 MKDLFATTEASSRKQEQRIVNYIKQHVELTNGNQIKKIEFIDFQKNEMTGTW  
GISTKINEQFSISFSEDRIGGKLRLALGYQPNEIGFSKDINSNNQNVNDIEVIYMK  
KE\*

40 Sequence description:

A] length: 333 bp - 111 aa (partial sequence)  
B] No obvious Shine Dalgarno sequence upstream  
of the ATG start codon, and no obvious signal  
peptide within the protein.



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10 ATGAAAAAACGTATATGGTATTTGATAATAATAATCACAGTAATTTTAGGA  
GGACTAGCCATGAAAAACTTATTTGCAACAACAGAAGCATCATCAAGGAA  
ACAGGAACAAGATAGAATTGTCAATTACATAAAACAACATGTTGAGTTAA  
CAAATGGTAATCAAATAAAAAAAATTGAGTTTATCGACTTTCAAAAAAAT  
GAGATGACAGGTACATGGGGAATTTCTACTAAAATTAATGAACAATTTTCG  
15 ATTAGTTTTTCTGAAGATAGAATTGGTGGTAAACTTAGAGCATTAGGATAT  
CAACCGAATGAAATAGGTTTTTCAAAGGACATCAATAGTAATAATCA  
  
MKKRIWYLIHITVILGGLAMKNLFATTEASSRKQEQDRIVNYIKQHVELTNGN  
QIKKIEFIDFQKNEMTGTWGISTKINEQFSISFSEDRIGGKLRALGYQPNEIGFSK  
20 DINSNNO

A] Length: 351 bp - 117 aa (Partial sequence)  
B] Obvious signal peptide and Shine Dalgarno  
sequence upstream of the ATG start codon.

ID-86

35 ATGTCAAATCAATATGATTATATCGTTATTGGTGGAGGTAGT  
GCAGGCAGTGGTACCGCTAATAGGGCAGCCATGTATGGAGC  
AAAAGTCCTGTTAATTGAAGGTGGACAAGTAGGTGGAACCTTG  
TGTAACTTAGGTTGTGTACCTAAGAAAATCATGTGGTATGG  
TGCACAAGTTTCTGAGACACTCCATAAGTATAGTTCAGGTTA  
40 TGGTTTTGAAGCCAATAATCCTTAGTTTTGATTTTACTACTCTA  
AAAGCTAATCGCGATGCTTACGTGCAGCGGTCTAGACAGTCG  
TATGCCGCTAATTTTGAGCGTAATGGGGTCGAAAAGATTGAT  
GGATTTGCTCGTTTTATTGATAACCATACTATTGAAGTGAATG  
GTCAGCAATATAAAGCTCCTCACATTACTATTGCAACAGGTG

GACACCCTCTTTACCCTGATATTATTGGAAGTGAACCTTGGTG  
AGACTTCTGATGATTTTTTTGGATGGGAGACCTTACCAAATTC  
TATATTGATTGTTGGGGCGGGCTATATCGCGGCAGAACTTGC  
TGGAGTGGTTAATGAATTAGGCGTTGAAACCCATCTTGCATT  
5 TAGAAAAGACCATATTCTACGCGGATTTGATGACATGGTAAC  
AAGTGAGGTTATGGCTGAAATGGAGAAATCAGGTATCTCTTT  
ACATGCTAACCATGTACCTAAATCTCTTAAACCGCATGAAGG  
TGGCAAGTTGATTTTTGAAGCTGAAAATGGGAAAACGCTTGT  
CGTTGATCGTGTAATATGGGCTATCGGCCGTGGACCAAATGT  
10 AGACATGGGACTTGAAAATACCGATATTGTTTTAAATGATAA  
AGATTATATCAAAACAGATGAATTTGAGAATACTTCTGTAGA  
TGGCGTGTATGCTATTGGAGATGTTAATGGGAAAATTGCCTT  
GACACCGGTAGCAATTGCAGCAGGTCGTCGCTTATCAGAAAG  
ACTTTTTAATCATAAAGATAACGAAAAATTAGATTACCATAA  
15 TGTACCTTCAGTTATTTTTACTCACCTGTAATTGGGACGGTA  
GGACTTTCAGAAGCAGCAGCTATCGAGCAATTTGGAAAAGAT  
AATATCAAAGTCTATACATCAACTTTTACCTCTATGTATACGG  
CTGTTACCAGTAATCGCCAAGCAGTTAAGATGAAGCTCATAA  
CCCTAGGAAAAGAGGAAAAAGTTATTGGGCTTCATGGTGTTG  
20 GTTATGGTATTGATGAAATGATTCAAGGTTTTTCAGTTGCTAT  
CAAAATGGGGGCTACTAAAGCAGACTTTGATGATACTGTTGC  
TATTCACCCAACCTGGATCTGAGGAATTTGTTACAATGCGCTA  
A  
25 MSNQYDYIVIGGGSAGSGTANRAAMYGAKVLLIEGGQVGGTC  
VNLGCVPPKIMWYGAQVSETLHKYSSGYGFEANNLSFDFTTLK  
ANRDAYVQSRQSYAANFERNGVEKIDGFARFIDNHTIEVNGQ  
QYKAPHITATGGHPLYPDIIGSELGETSDDFFGWETLPNSILIVG  
AGYIAAELAGVVNELGVETHLAFRKDHILRGFDDMTSEVMAE  
30 MEKSGISLHANHVPKSLKRDEGGKLIFEANGKTLVVDRVIWAI  
GRGPNVDMGLENTDIVLNDKDYIKTDEFENTSVDGVYAIGDVN  
GKIALTPVAIAAGRRLSERLFNHKDNEKLDYHNVPSVIFTHPVIG  
TVGLSEAAAIEQFGKDNIVYTSTFTSMYTAVTSNRQAVKMKLI  
TLGKEEKVIGLHGVGYGIDEMIQGFSAIKMGATKADFDDTVAI  
35 HPTGSEEFVTMR\*

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ID-87

ATGACAAAAAACAATCTTTAAACACGCTTGCTTGGCACTTACTACAGTATCA  
GTAGTGACATACAGCCAGGAGGTATATGGATTAGAAAGAGAGGAATCGGT  
CAAACAAGAACAAACCCAGTCAGCTTCAGAAGATGATTGGTTCGAAGAAG  
ATAATGAGAGGAAAACAATGTTTCTAAAGAGAATTCTACTGTTGATGAA  
ACAGTTAGTGATTTATTTTCTGATGGAAATAGTAATAACTCTAGTTCTAAA  
ACCGAGTCAGTGGTAAGTGACCCTAAACAAGTCCCCAAAGCAAAACCAGA  
GGTTACACAAGAAGCAAGCAATTCTAGTAATGATGCTAGCAAAGTAGAAG  
TACCAAAACAGGATACAGCTTCAAAAAAGGAACTCTAGAAACATCAACT  
TGGGAGGCCAAAAGATTTCTGTAAGTCTAGAGGGGATACTTTAGTAGGTTTTTCA  
AAATCTGGAATTAATAAGTTATCTCAAACATCACACTTGGTTTTTACCAAGT  
CATGCAGCAGATGGAAGTCAATTGACACAAGTAGCTAGCTTTTGCTTTTACT  
CCAGATAAAAAGACGGCCATTGCAGAATATACAAGTAGGCTAGGAGAAA  
ATGGGAAACCGAGTCGTTTAGATATTGATCAGAAGGAAATTATTGATGAG  
GGAGAAATATTTAATGCTTACCAGTTGACTAAGCTTACTATTCCAAATGGT  
TATAAGTCTATTGGTCAAGATGCTTTTGTGGACAATAAGAATATTGCTGAG  
GTTAACCTTCCTGAGAGTCTCGAGACTATTTTCAGACTATGCTTTTGCTCACA  
TGTCTTTTAAACAAGTAAAGTTACCAGATAACCTAAAGGTCATTGGAGAA  
TTAGCTTTTTTTGATAATCAGATTGGTGGTAAGCTTTACTTGCCACGTCCT  
TGATAAAATTAGCAGAACGCGCTTTCAAATCTAATCGTATTCAAACAGTTG  
AATTTTTGGGAAGTAAGCTTAAGGTTATAGGAGAAGCAAGTTTTCAAGAT  
AATAATCTGAGGAATGTTATGCTTCCGGATGGACTTGAAAAAATAGAATC  
AGAAGCTTTTACAGGAAATCCAGGAGATGAACATTACAACAATCAGGTTG  
TATTGCGCACAAGGACAGGCCAAAATCCACATCAACTTGCGACTGAGAAT  
ACTTACGTCAATCCGGACAAATCATTGTGGCGTGCAACACCTGATATGGAT  
TATACCAAATGGTTAGAGGAAGATTTTACCTATCAAAAAAATAGTGTTACA  
GGTTTTTCAAATAAAGGCTTACAAAAGGTAAGACGTAATAAAAACTTAGA  
AATTCAAAACAACACAATGGTATTACTATTACTGAAATTGGTGATAACGC  
TTTTTCGCAATGTTGATTTTCAAAGTAAACTTTACGTAAATATGATTTGGA  
AGAAATAAAGCTCCCCTCAACTATTCGGAAAAATAGGTGCTTTTGCTTTTCA  
ATCTAATAACTTGAAATCCTTTGAAGCAAGTGAAGATTTAGAAGAGATTA  
AAGAGGGAGCCTTTATGAATAATCGTATTGGAAGTCTAGACTTGAAAGAC  
AACTTATCAAAATAGGTGATGCTGCTTTCCATATTAATCATATTTATGCC  
ATTGTTCTTCCAGAATCTGTACAAGAAATAGGACGTTTCAGCTTTTCGACAA  
AATGGTGCGCTTACCTTATGTTTATCGGAAATAAGGTTAAAACAATTGGT  
GAAATGGCTTTTTTTATCCAATAAACTGGAAAGTGTAATCTCTCTGAGCAA  
AAACAATTAAGACAATTGAGGTCCAAGCTTTTTTCGGATAATGCCCTTAGT  
GAAGTAGTCTTACCGCCAAATTTACAGACTATTCGTGAAGAGGCTTTCAA  
AGGAATCATTTGAAAGAAGTGAAGGGTTCATCTACATTATCTCAGATTACT  
TTTAATGCTTTTGATCAAAATGATGGGGACAAACGCTTTGGTAAGAAAGTG  
GTTGTTAGGACACATAATAATTCTCATATGTTAGCAGATGGTGAGCGTTTT  
ATCATTGATCCAGATAAGCTATCTTCTACAATGGTAGACCTTGAAAAGGTT

TTAAAAATAATCGAAGGTTTAGATTACTCTACATTACGTCAGACTACTCAA  
 ACTCAGTTTAGAGAAATGACTACTGCAGGTAAAGCGTTGTTATCAAAATCT  
 AACCTCCGACAAGGAGAAAAACAAAAATTCCTTCAAGAAGCACAAATTTT  
 CCTTGGTCGCGTTGATTTGGATAAAGCCATAGCTAAAGCTGAGAAGGCTTT  
 5 AGTGACCAAGAAGGCAACAAAGAATGGTCATTTGCTTGAGAGGAGTATTA  
 ACAAAGCGGTATTAGCTTATAATAATAGTGCTATTAAAAAAGCTAATGTTA  
 AGCGCTTGGAAAAAGAGTTAGACTTGCTGACAGATTTAGTCGAGGGAAAA  
 GGACCATTAGCGCAAGCTACAATGGTACAAGGAGTTTATTTATTAAAGAC  
 GCCTTTACCATTGCCAGAATATTATATCGGATTGAACGTTTATTTTGACAA  
 10 GTCTGGAAAATTGATTTATGCACTTGATATGAGTGATACTATTGGCGAGGG  
 AAAAAAGATGCATATGGTAATCCTATATTAAATGTTGACGAGGATAATG  
 AAGGTTATCATACCTTGGCAGTTGCCACTTTAGCTGATTATGAAGGTCTTT  
 ATATTAAAGATATTTTAAATAGTTCCCTTGATAAGATTAAAGCAATACGCC  
 AGATTCCTTTGGCAAAATATCATAGATTAGGAATTTTCCAAGCTATCCGAA  
 15 ATGCAGCGGCAGAAGCAGACCGATTGCTTCCTAAGACACCTAAGGGGTAC  
 CTAAATGAAGTCCCAAATTATCGTAAAAAACAAATGGAGAAAAATTTAAA  
 ACCAGTTGATTATAAAACGCCGATTTTTAATAAGGCTTTACCTAATGAAAA  
 GGTAGACGGTGATAGAGCGGCTAAAGGTCATAATATAAATGCGGAGACTA  
 ATAATTCTGTAGCTGTAACACCAATAAGGTCCGAGCAGCAATTACATAAGT  
 20 CACAGTCTGATGTAAATTTACCTCAAACAAGTTCTAAAAATAATTTTATAT  
 ACGAGATTCTAGGATACGTTAGTTTATGTTTGCTTTTCTAGTAAGTCTGG  
 GAAAAAAGGAAAACGAGCAAGAAAAATAA

MTKKHLKTLALALTTVSVVTYSQEVYGLEREESVKQEQTQSASEDDWFEEDN  
 25 ERKTNVSKENSTVDETVDLFSFGNSNNSSSKTESVVSDDPKQVPAKPEVTQE  
 ASNSSNDASKVEVPKQDTASKKETLETSTWEAKDFVTRGDTLVGFSKSGINKL  
 SQTSHLVLP SHAADGTQLTQVASFAFTPDKKTAIAEYTSRLGENGKPSRLDIDQ  
 KEIIDEGEIFNAYQLTKLTIPNGYKSIGQDAFVDNKNIAEVNLPESLETISDYAF  
 AHMSLKQVKLPDNLKVIGELAFFDNQIGGKLYLPRHLIKLAERAFKSNRIQTV  
 30 EFLGSKLVIGEASFQDNNLRNVMLPDGLEKIESEAFNGPGEHYNNQVVLRL  
 TRTGQNPQLATENTYVNPDKSLWRATPDMDYTKWLEEDFTYQKNSVTGFS  
 NKGLQKVRNRKNLEIPKQHNGITITEIGDNAFRNVDFQSKTLRKYDLEEIKLPS  
 TIRKIGAFQSNLKSFEASEDLEEIKEGAFMNNRIGTLDLKD KLIKIGDAAFH  
 INHIYAIVLPESVQEIGRSAFRQNGALHLMFIGNKVKTIGEMAFLSNKLESVNL  
 35 SEQKQLKTIEVQAFSDNALSEVVLPPNLQTIREEAFKRNHLKEVKGSSTLSQITF  
 NAFDQNDGDKRFGKKVVVRTHNNSHMLADGERFIIDPKLSSTMVDLEKVL  
 KIEGLDYSTLRQTTQTQFREMTTAGKALLSKSNLRQGEKQKFLQEAQFFLGR  
 VDLDKAIKAEKALVTKKATKNHLLERSINKAVLAYNNSAIKKANVKRLEK  
 ELDLLTDLVEGKGPLAQATMVQGVYLLKTPLPLPEYYIGLNVYFDKSGKLIYA  
 40 LDMSDTIGEGQKDAYGNPILNVDEDNEGYHTLAVATLADYEGLYIKDILNSSL  
 DKIKAIRQIPLAKYHRLGIFQAIRNAAAEADRLLPKTPKGYLNEVPNYRKKQM  
 EKNLKPVDYKTPIFNKALPNEKVDGDRAAKGHNINAETNNSVAVTPIRSEQQL  
 HKSQSDVNLPQTSSKNNFIYEILGYVSLCLLFLVTAGKKGKRARK\*

## Sequence description:

- 5 A] Length 3168 bp - 1056 aa (Partial sequence)  
B] Obvious signal peptide with Shine Dalgarno  
sequence upstream of the ATG start codon.

10

ID-88

Clone RS-56

15

GCAGGATACATCATGCACAAGCACGAGGCTATCGTGTCATGCTGGGGTCA  
ACCCAGGAAGACATGTCGGCACAAGCTGAAGATTTCTTTACAGTCTGTACA  
CAATAAAGAGACGGGTAAGAGCGCTTTTAATGACAAAGAACGACTAGCAA  
20 TT

AGYIMHKHEAIVSCWGQPRKTCRHLKISLQSVHNKETGKSAFNDKERLAI

25

## Sequence description:

- A] Length:153 bp - 51 aa (partial sequence)  
B] No signal peptide visible, insufficient  
sequence data to determine the presence of a  
30 Shine Dalgarno sequence.

35 ID-89

Clone RS-58

GTGTCATTTATGCAAAGAAAATCCTATTTAAAATCCATGAGTGTTCTTACT  
40 TTAACAGCTTGTCTTATATCAGGATATGTGGTTAAAGATATTGCTATGTTA  
CATGCAGTATCTGCCAGTGAGAAGAAAGCAAATAATGTCAGTCCGAGAGA  
AAATCTCTACAGGGCTGTCAATGATAATTGGCTAGCCAATACAAAACCTCA  
AACAAGGGCAGACTAGTGTTAATAGTTTTTCAGAAATTGAGGATAAATTA  
AAGCAACTGTTAGTGTCTGATATGGCTAAAATGGCCTCAGGAAAGATTGA

AACAACCAATGATGAACAGAAAAAATGGTTGCATACTATAAACAAGGTA  
TGGACTTTAAAACAAGAGATAAAAAATGGTCTCAAACCTCTAAAACCAGTT  
TTACAAAAACTTGAAGCAGTCTCTTCAATGAAAGACTTTCAAAGTTTGGCC  
CATGATTTTGTGATGAGTGGTTTTGTTTTACCATTTGGTTTGACTGTGGAAA  
5 CCAATGCTCGAGATAATAGCCAAAAGCAATTGGTGCTTCGTCAAGCACCC  
GCATTACTTGAATCACCTGACCAATATAAGAAGGGCAATAAAGAAGGTGA  
GGCTAAATTATCAGCTTACCGTACTTCAGCAATGGCTTTGCTTAAACAAGC  
TGGAAAAAGTAACATTGAAGATAGAAAAGTAAACAAGCTATAGCAT  
TTGATAGACTCTTATCAGAAAAACGCAAGTTGATCAAAGTAAAATCACA  
10 GCTGAAAGTGAGACAGCTGCGGGGCGATATAACCCTGAAAGTATGGAAAC  
GGTTCACAATTACGCCAAGGAATTTGACTTTAAAGAATTGATTGAAAAACT  
AGTTGGGCCAACGAATAAGGCAGTCAATGTAGAAGATAAAAAGTATTTTA  
AACAGGTTAATGATGTTATAAATAGTAAACAATTAGCCAATATGAAAGCA  
TGGATGATGATTTCTATGCTAGTTGATCAATCAGATTTTCTAGGAGAACAA  
15 AATCGTCAAGCAGCGAGTGCTTTTAAGAATGTTGCGTCTGGTTTGACTCAG  
ATTGAATCGAAAGAAAAAATGCTTACACCCAATTAG

20 MSFMQRKSYLKSM SVLTLTACLISGYVVKDIAM LHAVSASEKKANNVSPREN  
LYRAVNDNWLANTKLKQGQTSVNSFSEIEDKLKQLLVSDMAKMASGKIETTN  
DEQKKMVAYYKQGMDFKTRDKNGLKPLKPVLQKLEAVSSMKDFQSLAHDF  
VMSGFVLPFGLTVETNARDNSQQLVLRQAPALLESPDQYKKGNKEGEAKLS  
25 AYRTSAMALLKQAGKSNIEDRKL VKQAIAFDRL LSEKTQVDQSKITAESETAA  
GRYNPESMETVHNYAKEFD FKELIEKL VGPTNKAVNVEDKTYFKQVNDVINS  
KQLANMKAWMMISMLVDQSDFLGEQNRQAASAFKNVASGLTQIESKEKMLT  
PN\*

30 Sequence description:

35 A] Length: 1095 bp - 365 aa (full length gene)  
B] an GTG (possible ATG start codon located 7 bp  
further downstream) start codon with an obvious  
signal peptide. Shine Dalgarno sequence present  
upstream of the ORF.

40 ID-90

Clone RS-59

ATGGAAATGCCTAAAAGAAATGAATTACTCAATAAAGAAATTTAAATGAG  
TATTGATAAACTTAGATATAAAGAACCAGAGAGTGAACATGACAAGCGAC  
CTACTTTTTATTTGGTAGTACTTATACTTGTTACTGTAGCAGTTATATTGTC  
GTTATTTAAATATTTTTTATAG

5

MEMPKRNELLNKEIKMSIDKLRYKEPESEHDKRPTFYLVVLILVTAVILSLFK  
YFL\*

10 Sequence description:

A] Length: 174 bp - 58 aa(full length gene)  
B] No obvious signal peptide, but Shine  
Dalgarno sequence is present upstream of ATG  
start codon.

15

20 ID-91

Clone RS-62 (partial sequence)

25

ATGCAGGTATTTTTAAATATTGTCAATAAATTCTTTGATCCAGTTATTCATA  
TGGGTTCCGGGAGTTGTGATGCTAATTGTCATGACAGGTTTAGCCATGATAT  
TTGGAGTGAAGTTTTCTAAAGCACTTGAAGGTGGTAT

30

MQVFLNIVNKFFDPVIHMGSGVVMLIVMTGLAMIFGVKFSKALEGG

Sequence description:

35

A] Length:141 bp - 41 aa (partial sequence  
B] Shine Dalgarno sequence present upstream of  
ATG start codon with a possible signal peptide  
present

40

ID-92

Clone RS-69 (partial sequence)

5 ATGAAAAAGAAAACATTCAGTGCTTATAACTTTTTAACGGCTCTTATCCTT  
TGTCTTTTGACAGTGCTTTTATCTTTCCATTTTATTGGATTATGACAGGAG  
CTTTTAA

MKKKTFSAYNFLTALILCLLTVLFIFPFYWIMTGAF

10

Sequence description:

15 A] Length: 110 bp -36 aa (Partial sequence)  
B] Possible signal peptide with Shine Dalgarno  
sequence directly upstream of the ATG start  
codon.

20

ID-93

Clone RS-70

25

30 ATGACTGAGAACTGGTTACATACTAAAGATGGTTCAGATATTTATTATCGT  
GTCGTTGGTCAAGGTCAACCGATTGTTTTTTTACATGGCAATAGCTTAAGT  
AGTCGCTATTTTGATAAGCAAATAGCATATTTTCTAAGTATTACCAAGTT  
ATTGTTATGGATAGTAGAGGGCATGGCAAAGTCATGCAAAGCTAAATAC  
CATTAGTTTCAGGCAAATAGCAGTTGACTTAAAGGATATCTTAGTTCATTT  
AGAGATTGATAAAGTTATATTGGTAGGCCATAGCGATGGTGCTAATTTAGC  
TTTAGTTTTTCAAACGATGTTTCCAGATATGGTTAGAGGGGCTTTTGCTTAAT  
35 TCAGGGAACCTGACTATTCATGGTCAGCGATGGTGGGATATTCTTTTAGTA  
AGGATTGCCTATAAATTCCTTCACTATTTAGGGAAACTCTTCCGTATATG  
AGGCAAAAAGCTCAAGTTATTTTCGCTTATGTTGGAGGATTTGAAGATTAGT  
CCAGCTGATTTACAGCATGTGTCAACTCCTGTAATGGTTTTGGTTGGAAAT  
AAGGACATAATTAAGTTAAATCATTCTAAGAACTTGCTTCTTATTTTCCA  
AGGGGGGAGTTTTATTCTTTAGTTGGCTTTGGGCATCACATTATTAAGCAA  
40 GATTCCCATGTTTTTAATATTATTGCAAAAAAGTTTATCAACGATACGTTG  
AAAGGAGAAATTGTTGAAAAAGCTAATTGA

MTENWLHTKDGSDIYYRVVGQGQPIVFLHGNSLSSRYFDKQIAYFSKYYQVIV  
MDSRGHGKSHAKLNTISFRQIAVDLKDILVHLEIDKVILVGHSDGANLALVFQ



TMFPDMVRGLLLNSGNLTIHGQRWWDILLVRIAYKFLHYLGKLFYPYMRQKA  
QVISLMLEDLKISPADLQHVSTPVMVLVGNKDIKLNHKKLASYPFRGEFYSL  
VGFGHHIIKQDSHVFNIIAKKFINDTLKGEIVEKAN\*

5

Sequence description:

- 10                   A] Length: 744 bp - 248 aa (full length gene)  
                  B] No obvious signal peptide, but Shine  
                  Dalgarno sequence upstream of the ATG start  
                  codon.

15

ID-94

20

Clone RS-71

25

ATGGTAGCAAAAGAGTTAGGTAAAAATAGCTTTACTATCCCAACTATTTGT  
TCTAATTGCTCCGCAGGTACTGCCATTGCAGTTGTATATAATGATGACCAT  
TCTTCTTAAGATACGGCTATCCCGAGTCTCCACTTCATATTTTTATCAATA  
CACGGATCATTGCACAGGCACCAAGCAAATATTTTTGGGCTGGTATTGGGG  
ACGGTATTTCAAAAGCCCCTGAAGTAGAACGTGCTACCTTAGAGGCTAAG  
ACCAATAAACTACCACATACTGCAGTGTTAGGACAAGCAGTCGCTCTGTCT  
TCAAAGGAAGCTTTTTATCAATTTGGTGAACAAGGTCTAAAAGACGTTGAA  
GCTAATTTAGCTTCGCGTGCAGTTGAAGAAATTGCGCTTGATATCTTA

30

MVAKELGKNSFTIPTICSNCSAGTAIAVVYNDHDSFLRYGYPEsplHIFINTRIIA  
QAPSKYFWAGIGDGISKAPEVERATLEAKTNKLPHTAVLGQAVALSSEAFY  
QFGEQGLKDVEANLASRAVEEIALDIL

35

Sequence description:

- 40                   A] Length: 405 bp - 135 aa (Partial sequence)  
                  B] No obvious Shine Dalgarno sequence upstream  
                  of the ATG start codon, probable signal  
                  peptide present at the N-terminus.

ID-95

## Clone RS-73

5 TTGAGGGAACTTACTGGAAAATTTCAAGCGATTGCGATAAAATAAATCTT  
 GCAGAGTTTTCTAGAGAAAGGAGGTCAGATTTATTGGAGTGGCAAGATCT  
 AGCGCAGTTACCTGTATCTATTTTTAAAGACTATGTTACAGATGCTCAAGA  
 CGCGGAAAAACCTTTTATATGGACAGAAGTATTTTAAAGGGAGATTAATCG  
 10 CTCAAATCAAGAAATTATTTTGCATATTTGGCCGATGACTAAGACAGTCAT  
 TCTGGGGATGTTAGATCGAGAATTACCACATTTAGAAATTAGCTAAAAAAG  
 AAATCATCAGTCGTGGTTATGAACCAGTTGTTTCGGAATTTTGGAGGTCTCG  
 CAGTTGTAGCTGATGAAGGAATTTTAAATTTTTCATTGGTTATTCCAGATGT  
 TTTTGAGAGAAAATTGTCTATCTCAGATGGGTATCTTATAATGGTCGATTTT  
 ATTAGAAGTATATTTTCGGATTTTATCAACCTATTGAGCACTTTGAAGTA  
 15 GAGACCTCCTATTGTCCTGGTAAGTTTGATCTTAGTATAAATGGCAAAAAA  
 TTTGCTGGCTTGGCTCAGCGCCGTATAAAGAATGGTATTGCGGTATCAATT  
 TACCTTAGCGTTTGTGGCGATCAAAAAGGGCGGAGTCAAATGATTTTCAGAT  
 TTTTATAAGATTGGTCTAGGTGATACGGGTAGTCCAATTGCTTATCCAAAT  
 GTAGATCCTGAAATTATGGCTAATCTATCTGATCTATTAGATTGTCCTATG  
 20 ACAGTAGAAGATGTTATTGATCGTATGTTGATTAGCCTTAAACAAGTAGGT  
 TTTAATGATCGTTTACTGATGATTAGACCCGATTTAGTTGCAGAGTTTGAT  
 AGATTTTCAGGCTAAGTCTATGGCTAATAAGGGGATGGTGAGCAGAGATGA  
 ATAA  
 25  
 MRETYWKISSDCDKINLAEFSRERRSDLLEWQDLAQLPVSIFKDYVTDAQDAE  
 KPFIWTEVFLREINRSNQEILHIWPMTKTVILGMLDRELPHLELAKKEIISRGYE  
 PVVRNFGGLAVVADEGILNFSLVIPDVFERKLSISDGYLIMVDFIRSIFSDFYQPI  
 30 EHFEVETSYCPGKFDLSINGKKFAGLAQRRIKNGIAVSIYLSVCGDQKGRSQMI  
 SDFYKIGLGD TGSP IAYPNVDPEIMANLSDLLDCPMTVEDVIDRMLISLKQVGF  
 NDRLLMIRPDLVAEFDRFQAKSMANKGMVSRDE\*

## Sequence description:

- 35 A] Length: 921 bp -307 aa (Full-length gene sequence)  
 B] No obvious Shine Dalgarno sequence upstream  
 of the TTG start codon or signal peptide  
 visible. Actual start point may be a further  
 40 85 bp downstream (TTG). This start point is  
 preceded by a typical Shine-Dalgarno sequence.

ID-96

Clone RS-74

5

TTGGAAGGTTTACTTATTGCATTGATTCCCATGTTTGC GTGGGAAAGTATT  
GGATTTGTTAGTAATAAAATTGGAGGGGCGTCCAAATCAACAAACATTTGG  
AATGACTTTAGGAGCATTGCTATTTGCGATTATCGTATGGTTATTTAAACA  
10 GCCAGAGATGACTGCCTCATTGTGGATTTTTGGTATCTTAGGTGGTATCCT  
ATGGTCAGTCGGCCAAAATGGTCAATTTCAAGCAATGAAATATATGGGAG  
TCTCTGTTGCTAATCCACTGTCAAGTGGTGCACAATTAGTAGGTGGAAGCC  
TAGTTGGTGCTTTAGTCTTTTCATGAATGGACTAAGCCAATCCAATTTATTTT  
AGGATTGACAGCGTTGACATTATTAGTTATCGGCTTCTATTTCTCAAGTAA  
15 ACGTGATGTTTCAGAACAAAGCTTTGGCAACACATCAAGAGTTTTTCAAAG  
GATTTGCTACAATTGCTTATTCAACTGTAGGTACATCTCGTACGCAGTTTTT  
ATTTAACAAACATTATGAAGTTCGACGCTATGGCCGTCATTTTACCCATGGC  
TGTTGGAATGTGTCTAGGTGCAATTTGTTTCATGAAGTTTCGTGTAACTTT  
GAGGCTGTTGTTGTTAAAAATATGATTACAGGTCTCATGTGGGGCGTTGGT  
20 AATGTCTTCATGTTATTGGCAGCAGCTAAAGCAGGGCTAGCAATTGCTTTT  
AGTTTTTCTCAACTTGGAGTAATTATCTCTATTATTGGTGGTATTTTATTTT  
AGGTGAGACAAAAACGAAGAAAGAGCAGAAATGGGTTGTCATGGGTATC  
CTTTGTTTTGTTATGGGTGCTATATTACTTGGTATTGTTAAATCTTATTAA  
25 MEGLLIALIPMFAWESIGFVSNKIGGRPNQQTFGMTLGALLFAIIVWLFKQPEM  
TASLWIFGILGGILWSVGQNGQFQAMKYMGVSVANPLSSGAQLVGGSLVGAL  
VFHEWTKPIQFILGLTALTLLVIGFYFSSKRDVSEQALATHQEFSKGFATIAYST  
VGYISYAVLFNNIMKFDAMAVILPMAVGMCLGAICFMKFRVNFEAVVVKNM  
TGLMWGVGNVFMLLAAAKAGLAIAFSFSQLGVIIISIGGILFLGETKTKKEQK  
30 WVVMGILCFVMGAILLGIVKSY\*

Sequence description:

35

A] Length: 867 bp - 289 aa (full-length gene)  
B] Possible Shine Dalgarno sequence upstream of  
GTG start codon, no obvious signal peptide  
present.

40

ID-97

Clone RS-75

5 ATGACAACCTTACTACGAAGCTATAAACTGGAACGAAATTGAAGATGTTAT  
 TGATAAATCAACTTGGGAAAACTAACCGAACAATTTTGGCTCGATACAC  
 GTATCCCTTTTATCAAATGACTTAGACGATTGGCGCAAACCTTCCGCTCAAG  
 AAAAAGATCTTGTGGCAAGGTTTTTGGAGGCTTAACCCTACTTGATACCA  
 TGCAATCAGAACTGGTGTGAAGCTATTCGTGCCGATGTTTCGCACGCCTC  
 10 ACGAAGAAGCTGTCTTAAACAATATTCAATTCATGGAATCTGTTACGCTA  
 AATCTTATTCTTCAATTTTCTCAACTTTAAATACTAAATCAGAAATTGAAG  
 AAATTTTCGAGTGGACTAATAATAATGAGTTCCTTCAAGAAAAAGCACGT  
 ATTATCAATGACATTTATGCTAATGGAAATGCCCTTCAAAAAAAGGTGGCT  
 TCCACCTACCTCGAAACCTTCCTTTTTTATTCTGGCTTTTTCACACCTCTTTA  
 CTATTTGGGAAATAATAAGTTAGCAAATGTTGCTGAAATCATTAAATTAAT  
 15 TATTCGTGATGAATCTGTACATGGTACTTATATCGGTTACAAATTCCAGCTT  
 GGTTTTAACGAATTACCAGAAGATGAGCAAGAGAATTTTCGTGATTGGAT  
 GTATGACCTCCTTTATCAGCTGTATGAAAACGAAGAAAAATACACCAAGA  
 CACTTTATGATGGCGTAGGATGGACTGAAGAAGTTATGACCTTTTACGCT  
 ACAATGCTAATAAAGCTCTTATGAATTTAGGACAAGATCCTTTATTCCCAG  
 20 ATACAGCAAATGATGTCAACCCAATTGTTATGAATGGTATTTCAACAGGAA  
 CATCAAACCATGACTTCTTCTCTCAAGTAGGTAATGGTTACCTACTTGGTA  
 GCGTTGAAGCTATGCATGATGATGACTATAACTATGGATTATAA

25 MTTYEAINWNEIEDVIDKSTWEKLTEQFWDTRIPLSNDLDDWRKLSAQEK  
 DLVGKVFGLTLLDTMQSETGVEAIRADVTPHEEAVLNNIQFMESVHAKSY  
 SSIFSTLNTKSEIEEIFEWTNNNEFLQEKARIINDIYANGNALQKKVASTYLETF  
 LFYSGFFTPLYYLGNKLANVAEIIKLIIRDESVHGTYIGYKFQLGFNELPEDEQ  
 ENFRDWMYDLYQLYENEEKYTKTLYDGVGWTEEVMTFLRYNANKALMNL  
 30 GQDPLFPDTANDVNPIVMNGISTGTSNHDFFSQVGNNGYLLGSVEAMHDDYN  
 YGL\*

Sequence description:

35 A] Length: 960 bp - 320 aa (full length gene)  
 B] Shine Dalgarno sequence present upstream of  
 ATG start codon, but no signal peptide  
 present.

40

ID-98

## Clone RS-77 (partial sequence)

5 ATGAATTGGTCACGTATCTGGGAACTCGTAAAAATTAATATCCTTTATTCA  
AACCCTCAGACTCTATCGGCACTAAGAAAAAAGCAAGAAAAGCATCCTAA  
AAAAGAATTTTCAGCTTATAAATCCATGTTTAGAAATCAGTTATTTTCAGAT  
TTTGCTCTTTTCAATAATTTATGTATTTCTCTTTGTATCACTTGATTTTAAAG  
AATATCCGGGCTATTTACAGTTCTACATTGGTATCTTTACACTAGTATCCAT  
10 TATCTACTCTTTTATTGCGATGTACAGTGTTTTCTATGAGAGTGACGATGTT  
AA

MNWSRIWELVKINILYSNPQTLSALRKKQEKHPKKEFSAYKSMFRNQLFQILL  
FSIIYVFLFVSLDFKEYPGYFTFYIGIFTLVSIISFIAMYSVVFYESDDV

15

## Sequence description:

- 20 A] Length: 311 bp - 103 aa (Partial sequence)  
B] Shine Dalgarno sequence present upstream of  
ATG start codon, no obvious signal peptide at  
N-terminus.

ID-99

25

## Clone RS-78 (partial sequence)

30 TAATCTTTTAGTCAACGGAGCAACAGGAAAATTGCAGGCTATGCGACAGA  
TATTCCACCACATAATTTAGCAGAAGTCATTGATGCTGTCGTGTACATGAT  
TGATCACCTAAAGCTAAATTAGATAAATTAATGGAATTTCTACCTGGTCC  
AGATTTTCCAACCTGGCGCTATCATTCAAGGAAAAGATGAAATTCGTAAGG  
CATATGAGACTGGTAAGGGGAGAGTAGCGGTTTCGCTCGCGAACTGCTATT  
35 GAAACCTTAAAAGGTGGTAAGAAACAAATTATTGTTACTGAAATTCCTTAT  
GAAGTTAAT

SFSQRSNRKIAGYATDIPPHNLAEVIDAVVYMIDHPKAKLDKLMEFLPGPDFPT  
GAIQGGKDEIRKAYETGKGRVAVRSRTAIETLKGGKKQIIVTEIPYEVN

40

## Sequence description:

- A] Length: 312 bp - 104 aa (Partial sequence)  
B] No obvious Shine Dalgarno sequence or a

signal peptide. Both N- and C- termini of ORF  
yet to be elucidated.

5 ID-100

Clone RS-79

10

ATGGGACGTAAGTGGGCCAATATTGTTGCCAAAAAGACTGCTAAAGATGG  
TGCTAACTCAAAAGTATACGCTAAATTCGGTGTGAAATATATGTTGCTGC  
AAAGCAAGGTGAACCAGACCCCGAGTCAAACCTCAGCTCTAAAATTCGTTT  
TGGACCGTGCTAAGCAAGCACAAAGTTCCAAAGCATGTTATTGATAAAGCG  
15 ATTGATAAAGCCAAAGGAAACACAGATGAAACTTTTCGTAGAGGGACGCTA  
TGAAGGTTTTGGTCCAAATGGTTCAATGATTATTGTGGATACTTTGACATC  
AAATGTTAACCGTACGGCAGCAAATGTACGTACTGCTTACGGTAAGAACG  
GTGGCAATATGGGAGCTTCAGGATCGGTATCCTACTTATTTGATAAAAAAG  
GTGTCATCGTTTTTGCTGGTGATGATGCTGACACTGTCTTCGAACAATTACT  
20 TGAAGCGGATGTAGACGTAGATGATGTTGAAGCAGAAGAGGGAACAATA  
ACAGTTTATACCGCCCCAACAGATCTTCATAAAGGTATCCAAGCACTTCGC  
GATAATGGTGTAGAAGAATTCCAAGTTACTGAACTTGAAATGATTCCTCAA  
TCAGAAGTAGTATTGGAAGGTGATGACCTTGAACTTTTGAAAAGCTT

25

MGRKWANIVAKKTAKDGANSKVYAKFGVEIYVAAKQGEPPDPESNSALKFVL  
DRAKQAQVPKHVIDKAIDKAKGNTDETFVEGRYEGFGPNGSMIIVDTLTSNV  
NRTAANVRTAYGKNNGNMGASGSVSYLFDKKGIVVFAGDDADTVFEQLLEA  
DVDVDDVEAEEGTITVYTAPTDLHKGIQALRDNGVEEFQVTELEMIPQSEVVL  
EGDDLETFEKL

30

Sequence description:

- 35 A] Length: 654 bp - 218 aa (Partial sequence)  
B] Possible Shine Dalgarno sequence upstream  
of ATG start, no obvious signal peptide

40 ID-101

Clone RS-80

TTGGAGAAATATTTGAAGAACCCGATTACATGGATTGGATTAGTTCTTGTG  
GTTACGTGGTTTTTAACTAAAAGTAGTGAATTTTTGATTTTTGGTGTGTGTG  
TCTTGTTGTTAGTATTTGCTAGTCAAAGTGAT

5

MEKYLKNPITWIGLVLVVTWFLTKSSEFLIFGVCVLLLVFASQSD

Sequence description:

10

A] Length: 135 bp - 45 aa (partial sequence)  
B] Shine Dalgarno sequence upstream of TTG  
start codon with possible signal peptide  
evident at N-terminus.

15

ID-102

20

Clone RS-81

ATGACACAATCAGATGCATATCTCTCGTTGAACGCGAAGACACGCTTTAGA  
GATCGCACAGGTAATTATCATTTTACTTCGGATAAAGAGGCTGTTGAACAA  
TATATGATAGAACATGTTGAACCTAATACGATGGTGTTCACATCACTAATT  
GAAAAGCTAGATTATTTGGTTTCTAATAACTACTATGAATCGGACCTTCTA  
AAACAATATAACCTTGAGTTTATTTGCCAAATTTTTGAGCATGCATACGCT  
AAGAAATTTGCTTTTCTAAATTTTATGGGGGCTTTAAAATTTTATAATGCTT  
ATGCTCTTAAT

25

30

MTQSDAYLSLNAKTRFRDRTGNYHFTSDKEAVEQYMIEHVEPNTMVFTSLIE  
KLDYLVSNYYESDLLKQYNLEFICQIFEHAYAKKFAFLNFMGALKFYNAYA  
LN

35

Sequence description:

40

A] Length: 318 bp - 106 aa (Partial sequence)  
B] Shine Dalgarno sequence present upstream of  
ATG start codon, no obvious signal peptide

ID-103

Clone 2-11A

5

ATGGTATTTATGGCAAATAAGAAAAAACAAGGAAAGAAAACCAGAA  
GACCTACTAAGGCAGAAATAGAGCGTCAAAGAGCTATTCAAAGGATGATT  
ACTGCTCTTGTTTTAACAATTATTCTCTTCTTTGGTATTATCAGATTAGGTA  
10 TTTTGGTATTACAGTCTATAACGTCATCCGTTTTATGGTAGGTAGCTTGGC  
TTACTTATTTATTGCGGCAACTTTAATCTACCTTTATTTCTTTAAATGGTTG  
CGAAAGAAAGATAGCTTAGTAGCAGGTTTTTGTATAGCTTCTTTAGGATTA  
TTGATTGAGTGGCATGCTTACCTTTTCTCAATGCCTATTTTGAAAGATAAA  
GAAATTTTTCGTTCAACTGCTCGATTAATTGTGTCTGATTTAATGCAATTTA  
15 AAATCACTGTTTTTGCCGGTGGAGGTATGTTGGGTGCTTTGATTTACAAGC  
CAATTGCTTTTCTCTTTTCTAATATTGGTGCCTATATGATTGGTGTCTCTTC  
ATCATTTTGGGTCTCTTTTAAATGAGTTCTCTGGAAGTTTATGACATCGTCG  
AATTTATTAGAGCTTTTAAAAATAAAGTGGCAGAGAAGCACGAGCAAAAT  
AAAAAGGAGCGTTTTGCTAAGCGAGAGATGAAAAAAGCAATCGCTGAACA  
20 AGAGCGCATAGAGCGTCAAAGCTGAAGAAGAAGCTTATTTAGCTTCGG  
TTAATGTAGACCCTGAAACGGGTGAGATTCTAGAGGATCAAGCTGAGGAC  
AATTTGGATGATGCGCTACCACCTGAGGTAAGTGAAACATCAACTCCGGT  
ATTTGAGCCAGAGATCCTTGCTTATGAGACATCGCCTCAAATGATCCTTT  
ACCAGTAGAGCCGACAATTTATTTAGAAGACTATGATTCGCCGATTTCCTAA  
25 TATGAGAGAAAATGATGAGGAAATGGTTTATGATTTAGATGATGATGTAG  
ATGATAGTGATATAGAAAATGTCGACTTTACACCTAAAACGCACTGGTTT  
ATAAATTACCAACGATAGATTTATTTGCACCAGATAAGCCTAAAAATCAAT  
CCAAAGAAAAGGATTTAGTCCGAAAGAATATCAGAGTTTTAGAAGAAACA  
TTTAGAAGTTTTGGTATCGATGTAAAAGTAGAACGTGCTGAAATTGGACCA  
30 TCAGTTACTAAATATGAAATTAAACCAGCAGTTGGAGTTCGTGTGAATCGT  
ATTTCAAATCTATCTGACGACCTAGCTCTTGCTCTTGACAGCAAAAGATGTG  
CGTATAGAAGCACCAATTCCTGGAAAATCATTAAATAGGTATTGAAGTTCCT  
AACTCAGAAATTGCAACGGTTTCTTTCCGCGAACTTTGGGAACAATCTGAT  
GCCAATCCTGAAAACCTTTTAGAAGTACCACTAGGAAAAGCTGTTAACGG  
35 CAATGCTCGCAGTTTTAACTTAGCTAGAATGCCGCATCTTTTGGTAGCTGG  
TTCAACTGGTTCAGGTAAATCTGTGGCAGTTAATGGAATTATTTCAAGTAT  
TTTGATGAAGGCACGTCCAGATCAAGTTAAGTTTATGATGATTGATCCCAA  
AATGGTTGAATTATCTGTTTATAATGATATTCCACATTTATTAATCCCTGTT  
GTAACCAATCCGCGTAAAGCAAGTAAGGCACTCCAAAAAGTTGTTGATGA  
40 AATGGAAAATCGATACGAGTTATTTAGCAAAATTGGTGTGCGTAATATAG  
CAGGTTATAATACAAAGGTTGAAGAGTTTAATGCTTCCTCTGAGCAAAAC  
AAATGCCTTTGCCTTTAATCGTTGTCAATTGTAGATGAATTGGCTGACTTGAT  
GATGGTTGCTAGTAAAGAAGTTGAAGATGCTATTATTCGTTTGGGGCAAAA  
AGCACGTGCTGCAGGTATCCATATGATTCTTGCAACTCAACGTCCATCCGT



AGATGTTATTTCTGGTTTGATTAAAGCAAATGTTCCGTCGCGTATTGCATTT  
GCTGTTTCAAGTGGTACTGATAGCCGTACGATCCTTGATGAAAATGGTGCT  
GAAAAGCTCTTGGGACGGGGTGACATGCTCTTTAAGCCTATTGATGAGAAT  
CATCCAGTACGACTACAAGGTTCTTTATTTTCAGATGATGATGTTGAAAGG  
5 ATCGTTGGTTTTATCAAAGACCAAGCCGAGGCTGACTATGATGATGCCTTT  
GATCCTGGAGAAGTATCTGAAACAGATAACGGCTCTGGTGGTGGCGGCGG  
AGTACCTGAAAGTGATCCTCTTTTTGAAGAAGCCAAGGGACTCGTTTTAGA  
GACGCAAAAAGCAAGTGCCTCAATGATTCAACGCCGATTGTCTGTTGGTTT  
CAATAGAGCAACAAGACTAATGGAAGAATTAGAAGCAGCGGGGGTTATTG  
10 GTCCAGCAGAAGGAACCAAGCCACGAAAAGTTTTAATGACTCCAACCTCCG  
AGTGAATAA

MVFMANKKKTKGKKTRRPTKAEIERQRAIQRMITALVLTIIFFGIIRLGIFGIT  
VYNVIRFMVGSLAYLFIAATLIYLYFFKWLRKKDSL VAGFLIASLGLLIEWHA  
15 YLFSMPILKDKEILRSTARLIVSDLMQFKITVFAGGGMLGALIYKPIAFLFSNIG  
AYMIGVLFILGLFLMSSLEVYDIVEFIRAFKNKVAEKHEQNKKERFAKREMK  
KAIAEQERIERQKAEEEEAYLASVNVDPETGEILEDQAEDNLDDALPPEVSETST  
PVFEPEILAYETSPQNDPLPVEPTIYLEDYDSPIPNMRENDEEMVYDLDDVD  
SDIENVDFTPKTTLVYKLPTIDLFAPDKPKNQSKEDLVRKNIRVLEETFRSFGI  
20 DVKVERAEIGPSVTKYEIKPAVGVRVNRISNLSDDLALALAAKDVRIEAPIPGK  
SLIGIEVPNSEIATVSFRELWEQSDANPENLLEVPLGKAVNGNARSFNLARMPH  
LLVAGSTGSGKSVAVNGISSLILMKARPDQVKFMMIDPKMVELSVYNDIPHLLI  
PVVTNPRKASKALQKVVDENENRYELFSKIGVRNIAGYNTKVEEFNASSEQK  
QMPLPLIVVIVDELADLMMVASKEVEDAIIRLGQKARAAGIHMILATQRPVSD  
25 VISGLIKANVPSRIAFAVSSGTDSTRITLDENGAEKLLGRGDMLFKPIDENHPVRL  
QGSFISDDDVERIVGFIKDQAEADYDDAFDPGEVSETDNGSGGGGGVPESDPL  
FEEAKGLVLETQKASASMIQRRLSVGFNRATRLMEELEAAGVIGPAEGTKPRK  
VLMTPTPSE\*

30

Sequence description:

35 A] Length: 2451 bp - 817 aa (Full-length gene)  
B] Shine Dalgarno sequence present upstream of  
ATG start codon, possesses a potential signal  
peptide

40 ID-104

Clone 2-18/22b

ATGTCACAAGAGCAAGGAAAAATTTATATTGTAGAAGATGATATGACGAT  
 TGTGTCACCTTTTAAAAGATCATTTATCAGCTAGCTATCATGTCTCTAGTGTC  
 AGCAATTTTCGTGATGTGAAACAAGAAATTATCGCATTTC AACCCGATTG  
 5 AACTAATGGATATTACGTTACCCTATTTTAATGGTTTTTACTGGACTGCAG  
 AATTGCGTAAGTTTTTAACAATTCCTATTATTTTCATTTTCATCTAGTAATGA  
 TGAAATGGATATGGTTATGGCATTAAATATGGGGGGTGATGACTTTATTTC  
 AAAACCATTCTCTCTAGCTGTATTAGATGCTAAGCTAACTGCTATTTTAAG  
 GAGAAGTCAACAATTTATCCAACAGGAATTAAGTTTTGGGGGATTACGTT  
 10 GACAAGAGAAGGGTTATTGTCTAGCCAAGATAAAGAGGTTATTTTATCGC  
 CAACAGAAAATAAAATCCTATCTATCTTGCTCATGCATCCTAAACAAGTAG  
 TCTCAAAAGAGTCTCTATTAGAGAACTTTGGGAAAATGATAGTTTTATTG  
 ATCAAAATACACTTAATGTTAATATGACACGCTTACGTAAAAAAATTGTCC  
 CAATAGGTTTTGATTACATTCATACAGTGAGAGGAGTTGGGTATTTACTAC  
 AATGA

15

MSQEQGKIYIVEDDMTIVSLLKDHLASYSYHVSSVSNFRDVKQEIIAFQPDILM  
 DITLPYFNGFYWTAELRKFLTIPFISSNDEMMDMVMALNMGGDDFISKPFSLA  
 VLDAKLTAILRRSQQFIQQLTFGGFTLTREGLLSSQDKEVILSPTENKILSILLM  
 20 HPKQVVSKESSLLEKLWENDSFIDQNTLVNMTRLRKKIVPIGFDYIHTVRGVG  
 YLLQ\*

Sequence description:

25

A] Length: 669 bp - 223 aa (full-length gene sequence)

B] Shine Dalgarno sequence present upstream of a GTG start codon.  
 Was not identified directly by LEEP. This gene was found upstream of  
 30 gene ID-10 described in WO 00/06736.

ID-105

35

Clone 2-20

ATGTATCAAACCTCAGACAAATAAGGAAAAATTTGTTTTATTTTTGAAATTA  
 TTTATCCCAGTATTGATTTATCAATTTGCTAATTTTTCAGCTACTTTTATTGA  
 40 TTCGGTTATGACTGGACAGTATAGTCAGCTACATTTGGCAGGTGTGTCAAC  
 TGCTAGTAATTTATGGACTCCGTTTTTCGCTTTATTAGTAGGTATGATTTCA  
 GCATTAGTACCAGTAGTTGGTCAACATTTGGGTAGAGGAAATAAAGAACA  
 AATTCGCACAGAATTTTCATCAATTTCTATATTTAGGTTTGATACTGTCCTTA  
 ATATTATTTTAAATCATGCAATTTATTGCTCAACCTGTCTTGGGGAGTTTGG

GTTTAGAAGATGAAGTTCTAGCAGTTGGTCGTGGTTATTTAAATTATATGT  
 TGATTGGAATCATGCCGCTGGTGTGTTTAGCATTTGCCGTTTCATTCTTTGA  
 TGCATTGGGGTTAACAAGGTTATCTATGTATCTGATGCTTTTAATTCTACCC  
 TTTAATTCATTTTTTAATTATATGCTTATCTACGGTAAATTTGGTATGCCTA  
 5 GACTAGGAGGTGCGGGGGCAGGTCTTGGAACCTTCTTTAACTTATTGGGGCTA  
 TTTTTATTGGTATTATTATTGTGATGTCACCTTCATCCTCAAATTAACATA  
 TCATATATGGACTCTGGAAAGAATAAAAGCTCCTTTGATTATTGAAGATAT  
 TCGATTGGGATTACCGATTGGTTTACAAATTTTTGCAGAAGTTGCAATTTTT  
 GCAGTAGTAGGCTTATTCATGGCAAAATTTCTTCAATCATTATTGCAGCA  
 10 CATCAGGCTGCTATGAATTTTTTCATCATTAAATGTATGCATTTCTTTAAGTA  
 TTTCCACTGCTCTAGCTATTACAATATCGTTTGAAGTAGGGGCAGAGCGCT  
 TTCAGGACGCAACCACTTATAGTAGGATAGGACGCTTAACAGCGGTAGGG  
 ATTACATCAGGAACCTTACTATTTTTATTTCTATTTTCGTGAGAATGTAGCAG  
 CAATGTATAATAGTGCCCTCACTTTGTCGCTATTACAGCTCAATTCCTAAC  
 15 TTATAGTCTCTTTTTCCAGTTTGCAGATGCTTATGCAGCTCCTGTACAGGGG  
 ATTTTACGAGGCTATAAGGATACAACAAAACCATTTATGATCGGTGCGGG  
 CTCTTATTGGTTATGTGCTTTGCCATTAGCGGTTATCTTAGAAAAAATAG  
 CCAGTTAGGTCCGTTTGCCTATTGGATTGGTTTAATCACAGGTATTTTTGTT  
 TGTGGTCTATTTCTAAACCAACGTCTGCAAAAGATTAAGAAGTTGTATTAT  
 20 TAA

MYQTQTNKEKFVLFLKLFIPVLIYQFANFSATFIDSVMTGQYSQLHLAGVSTAS  
 NLWTPFFALLVGMISALVPVVGQHLGRGNKEQIRTEFHQFLYLGLILSLILFLI  
 25 MQFIAQPVLGSLGLEDEVLA VGRGYLNYMLIGIMPLVLFISICRSFFDALGLTRL  
 SMYLMILLIPNSFFNYMLIYGKFGMPRLGGAGAGLGTSPTYWAIFIGIIIVMS  
 LHPQIKTYHIWTLERIKAPLIIEDIRLGLPIGLQIFA EVAIFA VVGLFMKFSSIIIA  
 AHQAAMNFSSLMYAFPLSISTALAITISFEVGAERFQDATTYSRIGRLTAVGITS  
 GTLLFLFLFRENVAAAMYSAPHFVAITAQFLTYSLFFQFADAYAAPVQGILRG  
 YKDTTKPFMIGAGSYWLCALPLAVILEKNSQLGPFAYWIGLITGIFVCGLFLNQ  
 30 RLQKIKKLYY\*

Sequence description:

35

A] Length: 1341 bp - 447 aa (full length gene)  
 B] Shine-Dalgarno sequence present upstream of  
 ATG start codon, There is a potential signal  
 peptide sequence

40

ID-106

## Clone 2-4A

5 TTGCTAGTTTCTTCTCTAGTTTCTTGTTCAATTTTTCTTGTCATTTTCGTCGTT  
GTCTTCATCAACACGAAATAAGTCTATAAACTTATCAAATAATTTTCATAGA  
CTTATTATATCAATTTTCAATAAAATGCTATAATAAAACCATGTCATTTTCA  
TTAAAAATTAGAAATCCATACGGTGAACATACCGTTAAAGAACTCCTTGA  
10 AGATTATTTTTTTGATTCCACGTAAGATTAGACATTTTTTTGCGTGTTAAAAAA  
CATGTACTTATAAACAATGAATTCATTAATTGGCAAACCTGTCGTCCAAGAA  
AACGATACTATTACCTTAATCTTTGATGATGAGGATTACCCTACTAAAAAA  
ATTCTCTGGGCAGAGCAGAGCTTATTGATTGTCTTTATGAGGATGAACAT  
CTTATTATCGTTAATAAACCTGAAGGTATGAAAACCTCACGGTAACCAACCA  
15 AATGAAATAGCACTGTTAAATCATGTATCTGCCTATTCTGGACAAACATGC  
TATGTTGTTTCATCGCCTAGATATGGAGACCAGTGGAGCTGTTTTATTTGCT  
AAAAATCCATTTATACTTCCCCTTATCAATCAACGCTTAGAACGAAAAGAA  
ATTTGGCGTGAATATTGGGCTTTAGTTGAAGGAAAATTTTCACCTAAGCAT  
CAAGTTTTTGAGAGACAAAATTGGACGGAACCGTCATGACAGACGTAAACG  
AATCATTGATTCTAAAAACGGTCAACATGCTATGACAATCATTGACGTTTT  
20 GAAGTATATCCAAAATAGTAGTCTCATAAAATGCCGACTGGAAACCGGAA  
GAACCCATCAAATTCGCATTCACTTATCTCATCACGGACATCCTTTAATAG  
GAGATCCCCTCTACAACCCTTCTTCTAATAATGAAAGGTTAATGCTACACG  
CTCACCGATTGACTCTATCCCATCCATTAACCTTGCGAACTATTAGCGTAG  
AGGCCCTTCATCTACTTTTCGAGAAGGTTTTAAACAATTATAAAAAAGGAG  
25 TTGGATAA

MLVSSLVSCSFFLVISSLSSSTRNKSINLSNNFIDLLYQFSIKCYNKTMSFSLKIR  
NPYGEHTVKELLEDYFLIPRKIRHFLRVKKHVLINNEFINWQTVVQENDTITLIF  
DDEDYPTKKIPLGRAELIDCLYEDEHLIVNKPEGMKTHGNQPNEIALLNHVSA  
30 YSGQTCYVVHRLDMETSGAVLFAKNPFILPLINQRLERKEIWREYWALVEGKF  
SPKHQVLRDKIGRNRHRRKRIIDSKNGQHAMTIIDVLKYIQNSSLIKCRLETG  
RTHQIRIHLSHHGHPLIGDPLYNPSSNNERLMLHAHRLTLSHPLTCETISVEAPS  
STFEKVLNNYKKGVG\*

35

Sequence description:

40

A] Length: 1029 bp - 343 aa (Full length gene sequence)  
B] No obvious Shine-Dalgarno sequence upstream  
of the putative TTG start codon. Possesses a  
potential leader peptide sequence.

ID-107

Clone 2-54

5

GAAGTAAATGCAACTCAACCTAATAATAGAACTACCTATATTATACCCGAA  
AGCAGTCATTCCATTGCAGAACACAGAGATTCCTGATAGAATCAAAGGG  
TTCTTCGGTTGCATTACTTAATAGCGATGAATTTAGAAAGACAGCGGGAGA  
10 GGATAGAGGTTTTGAAAGGGATAAGTTGAGGTCTTTGGATATCATTCCCTAA  
GGGAGATTTATCGACAAGTAATGTCATAGGTAATACGGACATTGCTAGTC  
AGATATCGTTGGGCTTTAAAAAGAATGCGATGCAGGAACACCATCTTACT  
AAAACATTCTCTCAAAAGGATGGAAAGTTATCGTCTGTTATAGAGGGGAT  
GCTTGCTATTGGCAAAGAGAAAGTAGAGAAAGAAATAAAATATAGTGGTA  
15 ATTTATGGCAAAAATTTAAAAGCTAAGGCACACTGCCTTGTTTGCTGTGTTG  
ATAATTTGAATTTTGAAGATATAAAATCTTATTTTCAATATTATTGTCATCT  
AAACCATCAGCTCAAATTACCTAAAGGTGCTATACTTTCTGCTAAAACAGA  
AGTATATAGGGGAGGAGATTTTGGGAGAAAAAATAAAGATAATGTGTTTG  
GTTACCGTATCCCCTCATTATTGAAAACCCAAAAAGGAACCTTTACTTGCGG  
20 GAGCTGATGAAAGAATTGAGCAAGCTTGTGATTGGGGAAACATAGGAATG  
GTTATTCGCCGTAGTGAGGATGATGGTGTCACTTGGGGAAAAAGAGAAAC  
TATTGTCAATCTCCGTAATAACCCTAGAGTTCGCTAGTTACTAGTGGTGA  
CTATAGTGGCTCACCTATTAATATGGATATGGCATTAGTTCAAGATACTAG  
CTCCAAGACGAAACGTATTTTTTCAATATATGATATGTTTCCAGAAGGAAG  
25 AGGCGTTATTAGTATTGCTAACACACCTGAAAAAGAATATACCCAAATCG  
GAGGACAGTCTTATCTTAATTTATATAATAATGGAAAGAAATCGAAGGTTT  
TACTATCCGTGACAAAGGTATTGTATATAATTTTAAAGGGAAAAAGACTG  
ATTATCATGTTATAACAGAACTACTAAAAGTGACCATTCAAATCTAGGGG  
ATATTTATAAGGGAAAAACAGCTACTTGGAATATATATTTTACAAAACATA  
30 AAACGTCACCATTTTCGTTTAGCAAAATCAAGCTATGTGTGGATGTCATATA  
GCGATGATGATGGTAGGACATGGTCATCACCTAGAGATATAACAGCAAGT  
CTTCGTCAGAAAGGCATGAAATTTTTGGGAATAGGACCTGGAAAAGGTAT  
AGTTTTAAATGGGGGCCACACGCTGGTCGTATTATTATTCCTGCCTATTCT  
ACGAATTGGAAATCTCATCTAAGAGGTTCACAATCTTCACGCCTAATTTAT  
35 TCAGACGACCATGGAAAAACGTGGCATACTGGAAAAGCAGTTAATGATAA  
CCGTATACTTTCTAATGGTGAAAAAATTCACCTCCTTAACAATGGATAATAA  
AAAAGAACAAAATACAGAATCCGTACCCGTTCAATTGAAAAATGGGGACA  
TTAAGTTATTTATGAGGAATCTAACTGGTAACCTAGAAGTAGCCACAAGTA  
AAGACGGCGGGGAGACTTGGCAAACCATGTTAAACGATATAAGGAAATT  
40 CATGATGCTTACGTCCAACCTATCAGCTATTCGCTTTGAGCATGACAAAAA  
GAGTATATTTTATTAGTGAATGCTAATGGGCCAGGGAAGAAGTGCCAAGA  
TGGATATGCACGTCTAGCGCAAGTTAATCGAAATGGTAGTTTTAAGTGGTT  
ATATCACCATCACATTCAAGATGGTTCGTTTGCTTACAACCTCTGTTCAACA  
ACTTAATAATGATCAATTTGGTGTCTTTATGAACATAGAGAAAAACATCA

AAATAGTTTTACTTTAAATTACAAAGTTTTTAAATTGGAGTTTTCTTAGTCAA  
AATACAGAGAAGCAAGGCACTTTATGGGAGAAAATGGCAGCAAATTGGCA  
TGTTTTGTTTAAATTTTATTTATGA

5

10

15

20

ELNATQPNNRTTYIIPESHSIAEQQRFLIESKGSSVALLNSDEFKRTAGEDRGF  
ERDKLRSLDIIPKGDSTSNVIGNTDIASQISLGFKKNAMQEHLTKTFSQKDG  
KLSSVIEGMLAIGKEKVEKEIKYSGNLWQKLKAKAHCLVCCVDNLNFEDIKS  
YFQYYCHLNHQLKLPKGAILSaktevyrGGDFGRKNKDNVFGYRIPSLLKTQ  
KGTLLAGADERIEQACDWGNIGMVIRSEDDGVTWGKRETIVNLRNNPRVPL  
VTSGDYSGSPINMDMALVQDTSSKTKRIFSIYDMFPEGRGVISIANTPEKEYTQI  
GGQSYLNLYNNGKSKSVFTIRDKGIVYNFKGKKTDYHVITETTKSDHSNLGDI  
YKKGQLLGNIYFTKHKTSPFRLAKSSYVWMSYSDDDGRTWSSPRDITASLRQ  
KGMKFLGIGPGKGIVLKWGPHAGRIIPAYSTNWKSHLRGSQSSRLIYSDDHG  
KTWHTGKAVNDNRILSNGEKIHSLTMDNKKEQNTESVPVQLKNGDIKLFMRN  
LTGNLEVATSKDGGETWQNHVKRYKEIHDAYVQLSAIRFEHDKKEYILLVNA  
NGPGKKCQDGYARLAQVNRNGSFKWLYHHHIQDGSFAYNSVQQLNNDQFG  
VLYEHREKHQNSFTLNYKVFNWSFLSQNTEKQGTLEWKMAANWHVLFKFYL  
\*

Sequence description:

- A] Length: 2052 bp - 684 aa (partial gene sequence)
- B] N-terminus has yet to be determined

25

ID-108

30

Clone 2-61

35

40

ATGCCTAAATTAATCGTATCTTTCCTCTGCATTTTATTATCCCTGACTTGTG  
TAAACTCTGTGCAAGCTGAAGAACATAAAGATATTATGCAAATTACCCGA  
GAAGCCGGATATGATGTTAAAGATATTAATAAACCTAAAGCGTCTATCGTT  
ATTGACAATAAAGGTCATATTTTGTGGGAAGATAACGCCGATTTAGAACGT  
GATCCCGCTAGCATGTCTAAAATGTTTACTTTATATTTACTATTTGAAGACT  
TAGCTAAAGGAAAAACAAACCTCAACACCACAGTGACTGCAACAGAAACA  
GACCAAGCCATAAGTAAGATTTATGAAATTAGTAATAACAATATTCATGCT  
GGGGTTGCTTATCCTATTCGTGAACTGATTACTATGACGGCTGTCCCGTCA  
TCTAATGTAGCAACTATTATGATTGCTAACCCTTATCACAAAACAATCCT  
GACGCCTTTATTAAACGAATCAATGAAACCGCCAAGAACTCGGTATGAC  
AAAACTCACTTTTATAACCCCAAGTGGGGCGGTAGCGAGTGCTTTTAAATGG  
ACTTTACTCCCCAAAAGAATACGATAACAATGCTACTAACGTTACGACTGC

ACGTGATCTATCAATTTTAACTATCATTTCCTTAAAAAATACCCTGATATA  
CTGAACTATACAAAATATCCTGAAGTCAAGGCCATGGTCGGAACCTCCTTAT  
GAAGAAACATTTACAACCTTATAACTACTCTACCCCCGGCGCTAAATTTGGA  
5 TTAGAAGGAGTAGATGGCTTAAAAACTGGTTCTAGCCCTAGCGCTGCTTTT  
AATGCCTTAGTTACAGCTAAACGCCAGAATACTCGCTTGATAACTGTGGTT  
TTAGGAGTTGGCGATTGGTCAGACCAAGACGGAGAGTACTATCGTCATCC  
GTTTGTCAACGCTCTTGTAGAAAAAGGTTTTAAAGACGCTAAAAATATTTT  
TTCTAAAACCTCCTGTATTAAAAGCCGTTAAACCTAAAAAAGAAGTTACTAA  
AACCAAAACCTAAATCTATTCAAGAACAGCCTCAAACAAAAGAACAGTGGT  
10 GGACAAAACAGATCAATTTATCCAATCACATTTTGTATCTATTTTAATTG  
TTCTGGGCACCATCGCTAGCCTTTGTCTTTTAGCTGGGATAGTATTACTTAT  
AAAGCGCTCTAGATAA

MPKLIVSFLCILLSLTCVNSVQAEHKDIMQITREAGYDVKDINKPKASIVIDN  
15 KGHILWEDNADLERDPASMSKMFTLYLLFEDLAKGKTNLNTTVTATETDQAI  
SKIYEISNNNIHAGVAYPIRELITMTAVPSSNVATIMIANHLSQNNPDFAIKRINE  
TAKKLGMTKTHFYNPAGAVASAFNGLYSPKEYDNNATNVTTARDLSILTYHF  
LKKYPDILNYTKYPEVKAMVGTPYEETFTTYNYSTPGAKFGLEGVDGLKTGS  
SPSAAFNALVTAKRQNTRLITVVLGVGDWSDQDGEYYRHPFVNALVEKGFK  
20 DAKNISSKTPVLKAVKPKKEVTKTKTSIQEQPQTKEQWWTKTDQFIQSHFVS  
ILIVLGTIASLCLLAGIVLLIKRSR\*

25 Sequence description:

30 A] Length: 1188 bp - 396 aa (full length gene)  
B] Shine Dalgarno sequence present upstream of  
ATG start codon, possesses a potential signal  
peptide

35 ID-109

Clone 45

40 ATGACTGAAAAATATTATAATTGGGCAACGCTTGGAACCGGCGTTATTGCC  
AACGAATTAGCCCAAGCACTGGAAGCACGTGGACAAAAATTATATTCTGT  
AGCTAATAGAACTTACGACAAAGGACTTGAATTTGCTAACAAATATGGTA  
TCCAAAAAGTTTATGATCACATAGATCAAGTATTTGAAGACCCTGAAGTGG  
ATATCATTTATATCTCTACTCCCCACAATACTCACATCTCATTTTTACGAAA

GGCTTTAGCAAATGGTAAGCACGTTCTTTGCGAAAAATCTATTACTTTAAA  
 TAGTACTGAGCTTAAAGAAGCCATAGATTTAGCCGAAACTAACCATGTTGT  
 CTTAGCTGAAGCCATGACTATTTTTCATATGCCAATTTACCGCCAATTTAAA  
 AACATTAGTTGATAGTGGAAAATTAGGACCGTTAAAAATGATTCAAATGA  
 5 ATTTTCGGAAGTTATAAAGAATATGATATGACTAACCGTTTTTTTCAGTCGTG  
 ACCTAGCAGGCGGTGCTTTGCTGGACATTGGTGTGTTATGCACTTTCTTGTAT  
 TCGCTGGTTTATGTCAGAAGCACCTCACAACATTACCTCTCAAGTTACATT  
 TGCACCAACAGGGGTTGATGAACAAGTTGGTATCCTACTAACCAACCCAG  
 CAAATGAGATGGCGACTGTCAGCCTTAGTTTACATGCAAAACAACCTAAA  
 10 CGAGCAACTATCGCTTACGATAAAGGCTACATTGAACTTTTTGAATATCCG  
 CGAGGACAAAAGGCAGTTATTACTTATACTGAGGATGGGCATCAAGATAT  
 TATCGAAGCTGGCAAAACTGAAAATGCTCTCCAATATGAGGTAGCTGATA  
 TGGAAGAAGCCATTTTCAGGAAAACTAACCACATGTACTTAAACTATAACC  
 AAAGATGTTATGGATATCATGACACAGCTACGTCAAGAATGGGGATTTAC  
 15 CTACCCAGAAGAAGAAAAATGA

MTEKYYNWATLGTGVIANELAQALEARQKLYSVANRTYDKGLEFANKYGI  
 QKVYDHIDQVFEDPEVDIIYISTPHNTHISFLRKALANGKHVLCESITLNSTEL  
 20 KEAIDLAETNHVVLAEAMTIFHMPYRQLKTLVDSGKLGPLKMIQMNFSGSYK  
 EYDMTNRRFFSRDLAGGALLDIGVYALSCIRWFMSEAPHNITSQVTFAPTGVDE  
 QVGILLTNPANEMATVSLSLHAKQPKRATIAYDKGYIELFEYPRGQKAVITYT  
 EDGHQDIIEAGKTENALQYEVADMEEAISGKTNHMYLNYTKDVMMDIMTQLR  
 QEWGFTYPEEEK\*

25 Sequence description:

30 A] Length: 984 bp - 328 aa (full length gene)  
 B] Shine Dalgarno sequence present upstream of  
 ATG start codon, possesses a potential signal  
 peptide

35 ID-110

Clone 2-2

40 GTGTATTCTCCTGTAAATCTTCTAAAGGAAAAGTGATATTGTTAAAAAGT  
 GATTTTCTAAAGAGCTTCATAGAAAGGAGAGGAAATATTTGTTTT  
 MYSPVKSSKGKVILLKSDFLKSFIERRGNICF



## Sequence description:

- 5                   A] Length: 96 bp - 32 aa (partial sequence)  
                  B] GTG start codon - no obvious Shine-Dalgarno  
                  sequence  
                  Possesses a potential signal peptide

10

ID-111

15       Clone 2-3

20                   AAATACTGTATCATTGCAACCTCAAATGCAGGTTTTGGAAACGAAGCATT  
                  ACAGGTGACAGCGATAAAGACTTGAAAATTATGGAACGAATTTCTCCATA  
                  TTTCCGTCCAGAATTTCTAAATCGTTTCAATGGTGTTATTGAATTCTCTCAC  
                  CTAAGCAAAGATGACTTAAGCGAAATTGTAGATTTGATGCTTGATGAAGTT  
                  AACCAAACAATTGGCAAAAAAGGAATTGACCTTGTGGTAGATGAAAATGT  
                  TAAATCACACTTAATTGAACTGGGTTATGACGAAGCAATGGGAGTACGTC  
                  CATTGCGCCGTGTCATCGAGCAAGAAATTCGAGATCGCATCACAGACTACT  
25                   ATCTCGATCATAACAGACGTTAAACACCTAAAAGCTAATTTGCAAGATGGCC  
                  AAATCGTCATTTCTGAAAGATAA

30                   KYCHATSNAFGNEAFTGDSKDLKIMERISPYFRPEFLNRFNGVIEFSHLKSD  
                  DLSEIVDLMLDEVNQTIGKKGIDLVVDENVKSHLIELGYDEAMGVRPLRRVIE  
                  QEIRDRTDYLDHTDVKHLKANLQDGQIVISER\*

## Sequence description:

- 35                   A] Length: 429 bp - 143 aa (partial sequence)  
                  B] N-terminus yet to be elucidated. This gene  
                  was not in frame with nuc

40

ID-112

Clone 2-5

ATGTCAATGAATTTTTCATTTTACCACAATATTGGTCCTATTTTAATTATG  
 GTGTGATGGTAACCATTATGATTTCAACATGTGTTGTTTTTTTGGAACTAT  
 TATAGGCGTGTTAATTGCTTTAGTAAAGCGTACTAATTTACATTTTCTCACA  
 ATATTAGCTAATTTCTATGTATGGGTATTTTCGTGGGACACCGATGGTAGTT  
 5 CAAATTATGATTGCTTTCGCATGGATGCATTTTAACAATTTACCAACAATT  
 AGCTTTGGTGTTTTAGATTTAGATTTTACACGACTTTTACCTGGTATCATT  
 TCATTTCCCTTAAATAGTGGTGCCTATATTTTCGGAAATTGTACGTGCAGGGA  
 TTGAGGCTGTACCATCTGGACAAATAGAAGCAGCTTACTCGTTGGGGATTC  
 GACCTAAAAATACACTTCGCTATGTTATCTTACCCCAAGCTTTTAAAAATA  
 10 TTTTACCTGCTCTAGGGAATGAATTTATTACAATTATTAAAGATAGTGCTCT  
 CCTTCAAACCTATTGGTGTTCATGGAATTATGGAACGGAGCACAATCAGTTGT  
 AACGGCTACTTACTCACCAGTTGCACCGTTATTATTTGCAGCATTTTACTAT  
 TTAATGTTGACAACGATTCTCTCAGCTTTGTTAAAACAAATGGAGAAATAT  
 CTTGGGAAAGGGGTAAAAATAGATGGTTGA  
 15 MSMNFSFLPQYWSYFNYGVMVTIMISTCVVFFGTIIGVLIALVKRTNLHFLTIL  
 ANFYVWVFRGTPMVVQIMIAFAWMHFNNLPTISFGVLDLDFTRLLPGIIISLNS  
 GAYISEIVRAGIEAVPSGQIEAAYSLGIRPKNTLRYVILPQAFKNILPALGNEFITI  
 IKDSALLQTIGVMELWNGAQSVVTATYSPVAPLLFAAFYYLMLTTILSALLKQ  
 20 MEKYLKGKGVKIDG\*

25 Sequence description:

A] Length: 699 bp - 233 aa (full length gene)  
 B] Shine-Dalgarno sequence preceded the 'ATG'  
 start codon. Possesses a potential leader peptide  
 sequence.

30

ID-113

35 Clone 2-7

ATGAAAGACCTATTACGAAATAGTCTAGAGCAAAGTGGAAATTTAAGTTT  
 TCAAGATATGATTTTACATATTCTTGTAGCAGCTTTATTGAGTGTAGTTATT  
 40 TATGTTTCCTATGCTTATACGCATAGTGGAAGTGCCTATAGTAAAAAGTTT  
 AATGTTTCATTAATGACATTGACGGTCTTGACTGCAACAGTAATGACCGTT  
 ATTGGTAATAATGTAGCCTTGTCATTGGGTATGGTCGGTGCCTTGTCAGTT  
 GTTCGTTTTAGGACAGCCATAAAAGATTCAAGAGATACAGTTTATATTTT  
 TGGACCATAGTTGTTGGTATCTGTTGTGGTGTTCGGTGACTATGTGGTAGCT

GCATTAGGAAGTAGCGTTATCTTTATCTTATTATGGGTTATGGGACGTGTT  
 AAAAACGAGAATCGTATGTTATTGATTGTGAAGTGCATAGAACACTAGA  
 AGTTGATTTAGAAAGGAATTTTCTTCCAATATTTTGACGGAAAAGCTGTTCA  
 GCGTGTTAAAAATTCAACAATACTATTGAAATGATTTTCGAAATCTC  
 5 TAGAAAAGATTACGATAAGCAACTCCATGTAGATAATCAGTTAACTGAAA  
 AAGTGTACCAATTGGGAAATATTGATTATTTCAACATTGTTAGCCAAAGCG  
 ACGAAATCAATGGGTAG

MKDLLRNSLEQSGNLSFQDMILHILVAALLSVVIYVSYAYTHSGTAYSKKFNV  
 10 SLMTLTVLTATVMTVIGNNVALSLGMVGALS VVRFRRTAIKDSRDTVYIFWTIV  
 VGICCGVGDYVVAALGSSVIFILLWVMGRVKNENRMLLIVKCDRTLEVDLEGI  
 FFQYFDGKAVQRVKNSTTNTIEMIFEISRKDYDKQLHVDNQLTEKVYQLGNID  
 YFNIVSQSDEING\*

15

Sequence description:

A] Length: 678 bp - 226 aa (full-length gene)  
 B] ATG start codon is preceded by a Shine-  
 20 Dalgarno sequence-Possesses a potential leader  
 peptide sequence

25

ID-114

Clone 2-8

AAAAATTCATTTTAGATTTCATTTTACGACTATATACTCAGAAGTACCAAAC  
 CTAATCCAAGGTTTGAAAAAAGAAAGAAGGAAGTCAGTATGACAACTAT  
 AAAAACAACCTTAAAGATGAGGCTATACGTGTTGAAGAGACAACAAAAGA  
 ATCATTTTACGATGTTGATATTGCCTTGTTTTTCAGCTGGTGGATCTATTTCA  
 GCAAAGTTCGCTCCTTATGCAGTAAAGTCTGGAGCAGTTGTAGTAGATAAC  
 35 ACGTCATATTTTCGTCAGAATCCTGATGTTCCACTAGTTGTTCCCTGAAGTAA  
 ATGCTCATGCCATGATTGGTCATAATGGTATCATAGCTTGTCCCAATTGTTT  
 TACTATTCAAATGATGATTGCTTTAGAGCCCATTCGTCAAAAATGGGGGAT  
 AGAGCGTGTTATAGTTTCCACCTATCAAGCTGTTTCGGGTTTCAGGTGCACG  
 TGCTGTTGAAGAACTAAGGAACAGTTGAGACAAGTTTT

40

KFILDSFYDYILRSTKPNPRFEKRKKEVSMTNYKNNFKDEAIRVEETTKESFYD  
 VDIALFSAGGSISAKFAPYAVKSGAVVVDNTSYFRQNPDPVPLVVPEVNAHAMI  
 GHNGIIACPNCSTIQMMIALEPIRQKWGIERVIVSTYQAVSGSGARAVEETKEQ  
 LRQV

## Sequence description:

- 5                   A] Length: 499 bp - 165 aa (partial sequence)  
                  B] N-terminus has yet to be determined

ID-115

10

Clone 2-9

- 15    ATGACAAATGAATTGATAATGCAAGCTTTTGAGTGGTATTTACCTAGTGAT  
      GGGAATCACTGGAAGAAATTAGAGGAGTCTATATCAGACCTTAAAAAACT  
      TGGAATTAGTAAAATCTGGTTACCACCAGCATTTAAGGGAAGTAGCAGTG  
      ATGATGTAGGATATGGTGTTTATGATCTCTTTGATTTAGGAGAATTTGACC  
      AGAATGGAACAATTAGAACAAAATATGGTAGGAAAGAAGAGTATCTAAA  
20    GCTTATTAAGTCGTTAAAGGCAAATGGCATTAAACCGTTTGCAGATATCGT  
      TCTTAACCATAAAGCCAATGGTGATCATAAAGAAAAATTTCAAGTCATCA  
      AAGTCAATCCTGAAAATCGTCAAGAAGCATTAAGTGAACCCTATGAGATT  
      GAAGGATGGACGGGATTTGATTTCCCAGGTAGACAGGGTGAGTACAATGA  
      TTTT  
25    MTNELIMQAFEWYLPDGNHWKKLEESISDLKKLGISKIWLPPAFKGTSSDDV  
      GYGVYDLFDLGEFDQNGTIRTKYGRKEEYLKLIKSLKANGIKPFADIVLNHKA  
      NGDHKEKFQVIKVNPNRQEALSEPYEIEGWTGFDFPGRQGEYNDF

30

## Sequence description:

- A] Length: 456 bp - 152 aa (partial sequence)  
                  B] ATG start codon is preceded by a Shine-  
35                Dalgarno sequence, no leader peptide sequence.

ID-116

40

Clone 2-10

ATGGAGGTTCTTATGAAGAAAGTGTTAGTAAGTAGTCTTTTGGTTTTAGGG  
 ATTACGATAACGTTACAACCAGTAGTTGAGGCTAAGGGGCCAAAAGTAGC  
 TTATACACAAGAGGGAATGACTGCTCTTTCGGACACAAATAAAGATAAAG  
 5 TCACTACTATTTCTATTGACGAGATTCAAAAAAGCTTAGAAGGTAAGAAGC  
 CGATTACTGTTAGTTTTGATATTGATGATACACTGCTTTTCAGTAGTCAATA  
 TTTTCAATATGGTAAAGAATATGTAACCTCCTGGATCGTTTGATTTTCTTCAT  
 AAACAAAAATTCTGGGATCTTGTTGCAAAACGAGGAGATCAAGATTCCAT  
 TCCCAAAGAATATGCTAAAAAATTAATTGCTATGCATCAAAAACGAGGAG  
 10 ATAAAATTGTTTTTATAACAGGTAGGACAAGAGGGTCAATGTATAAGGAG  
 GGCGAGGTTGATAAAACAGCTAAAGCCTTAGCTAAAGATTTTAAATTTGTA  
 CCATCTGAT

MEVLMKKVLVSSLLVLGITITLQPVVEAKGPKVAYTQEGMTALSDTNKDKVT  
 15 TISIDEIQKSLEGKKPITVSFDIDDTLLFSSQYFQYGKEYVTPGSFDFLHKQKFW  
 DLVAKRGDQDSIPKEYAKKLIAMHQKRGDKIVFITGRTRGSMYKEGEVDKTA  
 KALAKDFKFVPSD

Sequence description:

- 20 A] Length: 516 bp - 172 aa (partial sequence)  
 B] ATG start codon is preceded by a Shine-  
 Dalgarno sequence, Possesses a leader peptide  
 sequence.

25

ID-117

30 Clone 2-17

ATGCTTAAAAGATTATTTACTGAAGATGGGGAATTGACAAAGATTAGTCGT  
 35 CGTTTCGTTTGGATGTTAGTGGTTATCTATTGTCTTATTATTGTCAGGATGT  
 GTTTTGGGCCTCAAATTATGATTGAGGGGGTATCAACTCCGAATGTTTCAGC  
 GCTTCGGAAGAATTGTAGCTCTTTTAGTACCATTTAATTCTTTTCGTAGTTT  
 AGATCAGCTAACTAGCTTTAAAGAGATTCTTTGGGTTATTGGTCAAAATGT  
 AGTGAATATTTTACTGCTGTTTCCTCTCATTATAGGGTTACTATCCCTAAAG  
 CCAAGTTTACGGAAATATAAAAGCGTTATATTACTTGCTTTCTTGATGTCTC  
 40 TTTTCATAGAGTGTACTCAAGTTGTTTTAGATATTTTAATAGATGCTAATCG  
 GGTTTTTGAAATCGACGATCTATGGACAAATACCTTAGGCGGTCCTTTCGC  
 CCTATGGAGTTATCGAAACATAAAAGGTTGGCTTCTAACTATTAGAAAATG  
 A

MLKRLFTEDGELTKISRRFVWMLVVIYCLIIVRMCFGPQIMIEGVSTPNVQRFG  
RIVALLVPFNSFRSLDQLTSFKEILWVIGQNVVNILLFPLIIGLLSLKPSLRKYK  
SVILLAFLMSLFIECTQVVLDILIDANRVFEIDDLWTNTLGGPFALWSYRNIKG  
WLLTIRK\*

5

Sequence description:

- 10           A] Length: 516 bp - 172 aa (full-length gene)  
            B] ATG start codon is preceded by an Shine-  
               Dalgarno sequence. Possesses a potential leader  
               peptide sequence. C-terminus need further  
               confirmation.

15

ID-118

20           Clone 3-3

25           ATGAAAAAGCTTACTTTTATTTGGGATTTAGATGGGACATTAATAGATTTCG  
            TATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATTTTGGCTTA  
            ATATTTGATAAAGAATTAATCCATGAATATATTTTACAGGAATCAGTGGGG  
            CAATTATTGGTAAACCTTTCAGAGGAAGAGCAAATACCTCATGAAAAACT  
            GAAAGCATATTTTACAAAAGAACAAGAAAGTCGAGATTCTAAAATACATT  
            TAATGCCATATGCAAAAGAGATTTTAGAATGGACCAAAGAACAAGATATT  
            CCCAATTTTATGTATACACATAAAGGAGCAAGTACGCATTTCAGTGTGGA  
            ACCTTGCAGATCTCTCATTATTTTGATGAAATTTTAACTGGTGTTCGGGAT  
30           TCGAGCGAAAACCACATCCACAAGGGATTAATTATTTAGTTAAACGATATT  
            CTTTAGATAAATCAATGACTTATTACATAGGAGATCGTCCACTAGATTTGG  
            AGGTTGCTCAAAATGCTGGTATAAAATCCATAAACTTAAGGTTAGAGAATT  
            CCAAAGAAAACCTATAATATTTCAAGTCTCAAAGATATAATATCACTTGATT  
            TCACTCGTTTGGATTAA

35

            MKKLTFIWDLDGTLIDSYPIMEALEETYRHFGLIFDKELIHEYILQESVGQLL  
            VNLSEEEQIPHEKLKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTH  
            KGASTHSVLETLQISHYFDEILTGVSGFERKPHPQGGINYLVKRYSLDKSMTYYI  
            GDRPLDLEVAQNAGIKSINLRLNSKENYNISSLKDIISLDFTRLD\*

40

Sequence description:

- A] Length: 627 bp - 209 aa (Possible Full-length gene)

B] ATG start codon is preceded by an possible  
Shine-Dalgarno sequence. No obvious leader  
peptide sequence.

5

ID-119

10 Clone 3-7

ATGGAAAAAGAAAAAAATTAGGTCTTTTACCACTAACAATGCTTGTCATT  
GGCTCTCTTATCGGTGGCGGAATCTTTGATTTAATGCAAAATATGAGTTCC  
AGAGCCGGTTTGGTACCAATGCTTATTGCTTGGGTAACTACTGCTATCGGG  
15 ATGGGAACTTTCGTTTTAAGTTTTCAAAATTTATCTGAAAAAGGCCGGAC  
CTAACAGCTGGAATCTTTAGTTACGCTAAAGAGGGGTTTGGAACTTTATG  
GGATTTAACTCTGCATGGGGTTATTGGTTATCAGCTTGGCTTGGAAATGTT  
GCCTACGCTGCACTCTTATTCAGTTCACCTCGGTTATTTCTTTAAATTCCTTG  
GTAATGGAAATAATATCATCTCAATTATTGGAGCAAGTATAGTTATTTGGG  
20 TTGTCCATTTCTTAATTTTAAGAGGTGTTAATACAGCTGCATTTATTAATAC  
CGTAGTTACCTTTGCAAAATTAGTACCTGTTATTATTTTCTTAATTTACGCG  
TTATTAGCTTTCAAATTTAACATTTTTAGTCTTGATATCTGGGGAAATGGAT  
TACATCAATCAATTTTCAACCAAGTCAATTCAACTATGAAAACCGCTGTTT  
GGGTATTTATTGGTATTGAGGGCGCCGTTGTCTTCTCAGGTCGTGCTAAAA  
25 AACACTCTGATATTGGTAAAGCAAGTATCCTAGCATTATTCACCTATGATTT  
CACTTTATGTATTGATTTCTGTTTTATCACTTGGTATCATGTACAGTCCAGA  
ACTTGCAAACTTAAAAACACCAGCTATGGCTTACGTTCTAGAAAAAGCTGT  
TGGTCACTGGGGTGCTATCTTAGTTAACCTTGGTGTTATCATTTTCAGTATTT  
GGCGCTATTCTTGCTTGGACTTTATTTGCAGCAGAATTACCATATCAAGCT  
30 GCTAAAGAAGGTGCTTTTCTAAATTTTTTGCAAAAGAAAAATAAAAAACAA  
AGCTCCAATCAACTCACTCTTAGTCACTAATCTTTGTGTACAAGCATTCTTA  
ATCACGTTCTTATTCACACAAAGTGCTTATCGTTTTGGTTTTCGCATTAGCAT  
CATCTGCTATCTTAATTCCTTATGCTTTTACAGCACTATATCAATTACAATT  
CACACTCCGTGAGGATAAGTCAACTCCAGGACATCAAAAGAATTTAATTA  
35 TCGGTATCCTCGCTACAATCTATGCTGTTTACCTTATCTACGCTGGTGGTTT  
TGATTACTTACTTTTGACAATGATTGCTTATACTCTAGGTATGATTCTCTAT  
ATTAAAATGAGAAAAGATGACAAGCTTGGCGTAATCATGGTCATAGCTGT  
TTCCAGTGTGAAATTGTTATCC

40

MEKEKKLGLLPLTMLVIGSLIGGGIFDLMQNMSSRAGLVPMLIAWVITAIGMG  
TFVLSFQNLSEKRPDLTAGIFSYAKEGFGNFMGFNSAWGYWLSAWLGNVAY  
AALLFSSLGYFFKFFGNGNNIISIIGASIVIWVVHFLILRGVNNTAAFINTVVTFAK  
LVPVIIFLISALLAFKFNIFSLDIWGNGLHQSFNQVNSTMKTAVWVFIGIEGAV

VFSGRAKKHSDIGKASILALFTMISLYVLISVLSLGIMSRPELANLKTPAMAYV  
LEKAVGHWGAILVNLGVIIISVFGAILAWTLFAAELPYQAAKEGAFPKFFAKEN  
KNKAPINSLLVTNLCVQAFLITFLFTQSAYRFGFALASSAILIPYAFTALYQLQF  
5 TLREDKSTPGHQKNLIIGILATIYAVYLIYAGGFDYLLLTMIAYTLGMILYIKMR  
KDDKLGVMVIAVSSVKLLS

Sequence description:

10

A] Length: 1356 bp - 452 aa (partial sequence)  
B] ATG start codon is preceded by an possible  
Shine-Dalgarno sequence. Possesses a potential  
leader peptide sequence.

15

ID-120

20

Clone 3-8

25 ATGAAATTTGAAAAACGGCAGGTCTATTATGTTGTCATAACATTTGCTATT  
TGCTATGCTATACAGGCTTATTGGGGAGCTGTTTCTAATATTTTAACTACGC  
TTCATAAGGCAATATTTCTTTTTTGGATGGGAGCTGGAATTGCCTATATTAT  
TAATATTGTAATGTCAGTCTATGAGCGATTATATATAAAGCTTTTTAAAGG  
ATCTAGACTATTAATGGCAATCAAGCGTAGTGTTTCTATGATTTTATCCTAT  
GCAACTTTTATTGGTTTAATTGTCTGGCTATTTTCAATTGTCATTCCAGATT  
30 TGATTTCTAGTTTGAGTTCCTTATTGGTTATTGATACCGGAGCACTTGCTAA  
ATTGGTTAATAATCTCAATGAAAATAAACAAATTTCTGAGGCTTTAAATTA  
TATGGGAACAGATAAAGACTTAGTTTCTACTTTAAGTGGTTATAGCCAGCA  
GATTTTGAAGCAAGTTTTATCTGTTTTTAACAAATTTACTAACCTCAGTTTCC  
TCTATTGCGGCAACACTTCTGAATGTTTTTGTAGTTTTATTTTTTCAATTTA  
35 CGTTTTGGCAAACAAGGAGCAGTTGGGACGTCAATTTAATTTGTAAATTGA  
TACCTATTTAGGTTCAACAGGCAAAACATTCCATTACGTTTCGTCATATCCTT  
CATCAACGTTTCCATGGTTTTTTTTGTAAGCCAAACTTTAGAAGCTATGATTT  
TAGGAAGTTTGACGGTTATTGGTATGTTGATCTTCCAATTTCTTATGCTTT  
AACAGTTGGGGTTTTAGTTGCTTTTACAGCTCTAATACCGGTTGTGGGAGC  
40 CTACATTGGTGTTACAATCGGTTTCATCTTAATTGCTACTGAATCGCTTACT  
GAAGCATTCTTGTTTGTCTTTTCTTGATCCTTTTACAACAATTTGAGGGAA  
ATGTCATTTATCCGAAAGTTGTCGGTGGATCGATTGGACTGCCTTCTATGT  
GGGTTTTAATGGCTATTACTATCGGAGGTGCTTTATGGGGGATCTTAGGCA



TGTTACTTGCTGTTCCCTGTTGCAGCTACTATCTATCAGATTGTAAAAGATCA  
TATTATCAAGCGACAAACGCTTAGAAATCGTGCACGAACCTATCGTTAA

5 MKFEKRQVYYVVITFAICYAIQAYWGAVSNILTTLHKAIFPFLMGAGIAYIINI  
VMSVYERLYIKLFLKGSRLMAIKRSVSMILSYATFIGLIVWLFSIVIPDLISLSS  
LLVIDTGALAKLVNNLNENKQISEALNYMGTDKDLVSTLSGYSQQILKQVLSV  
LTNLLTSVSSIAATLLNVFVSFIFSIYVLANKEQLGRQFNLLIDTYLGSTGKTFH  
YVRHILHQRFHGFFVSQTLEAMILGSLTVIGMLIFQFPYALTVGVLVAFTALIP  
10 VVGAYIGVTIGFILATESLTEAFLFVLFLILLQQFEGNVIYPKVVGGSIGLPSM  
WVLMAITIGGALWGILGMLLAVPVAATYQIVKDHIIKRQTLRNRARTYR\*

Sequence description:

15 A] Length: 1134 bp - 378 aa (full-length gene)  
B] ATG start codon is preceded by an typical  
Shine-Dalgarno sequence. Possesses a potential  
leader peptide sequence.

20

ID-121

Identical to ID-68, as described in WO 00/06736

25

ID-122

30

Clone 3-16

35 GTGATTACAATTAAAAAGGAATCTGTTATCAAACCTATTGAAGTATGCTTTT  
GGCATTATAATGGGATTTATTATCTTAGCTATTGTAATAGGTGGGCTCCTA  
TTTGCATACTACGTTAGTCGTTCTCCGAAATTAACCGATCAAGCTTTAAAA  
TCCGTTAACTCTAGTTTGGTTTATGATGGTAATAATAAACTTATTGCCGATT  
TAGGCTCAGAAAAGCGTGAAAGTGTTAGTGCGGATAGCATTCCACTAAAT  
TTGGTTAACGCTATCACTTCTATAGAAGATAAACGTTTCTTTAAACATAGA  
40 GGTGTCGATATTTATCGTATTTTAGGTGCAGCTTGGCATAACCTTGTTAGTA  
GTAATACGCAAGGTGGTTCAACCCTTGATCAACAGTTGATTAACTGGCTT  
ACTTTTCTACCAATAAATCTGACCAAACGTTAAACGTAATCACAGGAA  
GTTTGGCTTGCGCTTCAAATGGAGCGTAAATACACCAAAGAAGAAATTCTT  
ACTTTCTATATTAATAAAGTTTATATGGGAAATGGGAATTATGGTATGAGA

ACAACAGCTAAATCATACTTTGGTAAAGACCTAAAGGAATTATCTATTGCA  
CAACTTGCTTTGCTCGCTGGTATTCCTCAAGCACCTACACAATATGACCCTT  
ATAAAAACCCAGAATCTGCTCAAACAAGACGTAATACCGTTCTTCAGCAG  
ATGTATCAAGATAAAAACATTTCTAAAAAGGAATACGACCAAGCTGTTGC  
5 AACTCCAGTAACTGATGGCTTAAAAGAATTAAAGCAAAAATCTACTTATCC  
AAAATATATGGATAACTACTTAAAACAAGTTATTAGTGAAGTTAAACAAA  
AACTGGTAAAGATATCTTTACTGCTGGGCTAAAAGTGTATACTAATATCA  
ACACTGATGCACAAAAACAATATATGACATCTACAACAGTGATACTTAC  
ATCGCTTATCCAAACAATGAATTACAAATAGCATCTACCATCATGGATGCG  
10 ACTAATGGTAAAGTCATTGCACAATTAGGCGGGCGTCATCAGAATGAAAA  
TATTTTCAATTTGGGACAAATCAATCTGTCTTAACAGACCGCGATTGGGGTTC  
TACAATGAAACCTATCTCAGCTTATGCACCTGCTATTGATAGTGGTGTCTA  
TAATTCAACAGGTCAATCATTAAACGACTCAGTTTACTACTGGCCTGGTAC  
TTCTACTCAACTATATGACTGGGATCGTCAATATATGGGTTGGATGAGTAT  
15 GCAGACCGCTATTCAACAATCACGTAACGTCCCTGCTGTCAGAGCACTTGA  
AGCCGCTGGATTAGACGAAGCAAAATCTTTCCTTGAAAAATTAGGCATAT  
ACTATCCAGAAATG

MITIKKESVIKLLKYAFGIIMGFILAIIVIGLLFAYYVSRSPKLTQALKSVNSS  
20 LVYDGNNKLIADLGSEKRESVSADSIPLNLVNAITSIEDKRFFKHRGVDIYRILG  
AAWHNLVSSNTQGGSTLDQQLIKLAYFSTNKSQTLKRKSQEVWLALQMER  
KYTKEEILTFYINKVYMGNGNYGMRTTAKSYFGKDLKELSIAQLALLAGIPQA  
PTQYDPYKNPESAQTRRNTVLQQMYQDKNISKKEYDQAVATPVTDLKELK  
QKSTYPKYMDNYLKQVISEVKQKTGKDIFTAGLKVYTNINTDAQKQLYDIYN  
25 SDTYIAYPNNELQIASTIMDATNGKVIAQLGGRHQENISFGTNQSVLTDRDW  
GSTMKPISAYAPAIDSGVYNSTGQSLNDSVYYWPGTSTQLYDWDQRQYMGWM  
SMQTAIQQSRNVPVRALEAAGLDEAKSFLEKLGIIYPEM

30 Sequence description:

A] Length: 1386 bp - 462 aa (partial sequence)  
B] GTG start codon is preceded by an  
35 typical Shine-Dalgarno sequence. Possesses a  
potential leader peptide sequence.

40 ID-123

Clone 3-17

ATGGCTAATGTATATGATTTAGCAAATGAATTAGAACGTGCTGTTCGTGCT  
TTACCAGAATACCAAGCAGTTTTAACTGCAAAAGCAGCTATTGAAAATGA  
TGCGGATGCACAAGTGCTTTGGCAAGACTTTTTGGCTACCCAATCAAAAGT  
TCAAGAAATGATGCAATCTGGCCAAATGCCAAGTCAAGAAGAACAAGATG  
5 AAATGTCTAAACTTGGGGAAAAAATTGAATCCAATGACCTTTTAAAAGTTT  
ATTTTGACCAACAACAACGGTTGTCTGTCTATATGTCTGATATCGAAAAAA  
TTGTCTTTGCACCCATGCAGGACTTGATGTAA

MANVYDLANELERAVRALPEYQAVLTAKAAIENDADAQVLWQDFLATQSK  
10 VQEMMQSGQMPSQEEQDEMSKLGEKIESNDLLKVYFDQQRLSVYMSDIEKI  
VFAPMQDLM\*

Sequence description:

15 A] Length: 336 bp - 112 aa (full length sequence)  
B] ATG start codon is preceded by an  
typical Shine-Dalgarno sequence. No obvious  
potential leader peptide sequence.

ID-124

25 Clone 3-26

ATGGCAGAAATCACAGCTAAACTTGTAAAAGAATTGCGTGAAAAATCAGG  
30 TGCAGGCGTTATGGACGCTAAAAAAGCATTAGTAGAACTGATGGTGACC  
TTGATAAAGCGATTGAATTACTTCGCGAAAAAAGGTATGGCTAAAGCAGCT  
AAAAAAGCAGACCGTGTTGCTGCTGAAGGTTTAACAGGTGTTTATGTTGAT  
GGTAACGTTGCAGCAGTTATTGAAGTTAA

35 MAEITAKLVKELREKSGAGVMDAKKALVETDGDLDKAIELLREKGMAKAAK  
KADRVA AEGLTGVYVDGNVAAVIEV

Sequence description:

40 A] Length: 230 bp - 76 aa (partial sequence)  
B] ATG start codon is preceded by an  
typical Shine-Dalgarno sequence. No obvious  
potential leader peptide sequence.

ID-125

5

Clone 3-33

10 ATGATAAAAAACCTGTTATTAACAGGTTTTTTATCATTTAATGACGGAAAA  
CTGGACACAAATTATTTTTCTTGTATAATTAAATATATTATTTCTTATCAGG  
AGGTTATGATGACATTAGAGAAACGATTAA

15 MIKNLLLTGFLSFNDGKLDTNFYFSCIHKYIISYQEVMMTLEKRF

Sequence description:

20 A] Length: 134 bp - 44 aa (partial sequence)  
B] ATG start codon is preceded by an  
typical Shine-Dalgarno sequence. Possible  
potential leader peptide sequence.

25

ID-126

Clone 3-41

30

ATGAAAAATAATAAAAAATAATGGTTTTCTGAAAAATTCCTTTATTTACATA  
TTATTGATTATTGCGGTTATTACAACCTTTCAATACTATTTAA

35 MKNNKNNGFLKNSFIYILLIHAVITTFQYYL

Sequence description:

40 A] Length: 94 bp - 31 aa (partial sequence)  
B] ATG start codon is preceded by a  
possible Shine-Dalgarno sequence. Potential  
leader peptide sequence.

ID-127

5

Clone 3-42

10 ATGTTAGATATTATCTTATCCGGAATTTTCGCAAGGATTACTTTGGTCAATTA  
TGGCAATTGGCGTGTTTATCACTTTTCGTATCTTAGACATAGCCGATCTCTC  
TGCAGAAGGGGCTTTCCCTATGGGGGCTGCAGTTTGCGCCTTATGTATCGT  
TAA

15 MLDIILSGISQGLLWSIMAIGVFITFRILDIADLSAEGAFPMGAAVCALCIV

Sequence description:

20 A] Length: 158 bp - 52 aa (partial sequence)  
B] ATG start codon is preceded by a  
possible Shine-Dalgarno sequence. Potential  
leader peptide sequence.

25

ID-128

30 Clone 3-43

35 ATGGAAATGCCTAAAAGAAATGAATTACTCAATAAAGAAATTAATAATGAG  
TATTGATAAACTTAGATATAAAGAACCAGAGAGTGAACATGACAAGCGAC  
CTACTTTTTATTTGGTAGTACTTATACTTGTTACTGTAGCAGTTATATTGTC  
GTTATTAA

MEMPKRNELLNKEIKMSIDKLRYKEPESEHDKRPTFYLVVLILVTAVILSLF

40 Sequence description:

A] Length: 161 bp - 53 aa (full-length gene)  
B] ATG start codon is preceded by a  
possible Shine-Dalgarno sequence. Potential

leader peptide sequence.

ID-129

5

Clone 3-44

10 GTGGTAAGTAAATTGAGTTTAACAACGATTTTTGCATTGCTATTTTCATCA  
ATGCTAATTTACGCAACACCTCTTATCTTTACAAGTATTGGGGGAACCTTC  
TCTGAACGTGGTGGTATCGTCAACGTTGGTTTAGAAGGAATTATGGTAATT  
GGAGCTTTCTCAGGCGTTGTATTTAA

15 MVSKLSLTTIFALLFSSMLIYATPLIFTSIGGTFSEKGGIVNVGLEGIMVIGAFSG  
VVF

20 Sequence description:

A] Length: 179 bp - 59 aa (partial sequence)

B] GTG start codon is preceded by a  
possible Shine-Dalgarno sequence. Potential  
leader peptide sequence.

25

ID-130

30

Clone 3-46/47

35 ATGAGAATTATTGCAATAACTGAAAAGGTTATAAAAGAACTGTTTCGTGAT  
AAAAGAACACTTGCTATGATGTTTTTAGCACCTATTTTAATTATGTTTTTGA  
TGAATGTTATGTTTTCTGCGAATAGTAATACAAAAGTTAAGATTGGAACATA  
TTAACGTTAACACGAAGGTCGTTTCAAATTTAGATAATATTAAGCATATTC  
AAGTGAGATCATTTAAATTTAACTCATCTGCTAAAAAAGCACTCAAATCAA  
ATAAAATTGATGCTCTTATTTTCGGAGGACAATAAATCTTATACTGTCTTCT  
40 ATGCGAATACAGATTCTTCAAAGACGACTTTAACAAGACAAGCTTTTAAA  
ACCGCTGTTAATAACAATGAACAGTAAGGAACTGATTTTCGCAAGTTAAAATT  
TTAGCTAATAAGAATCCGAACTAGCACAATCCTTACAACTCGCTCCAAA  
TATATCAAAGAAAAATATAATTACGGAAATAAAAAATACAGGCTTTTTTGC  
AAAAATGATACCAATACTAATGGGATTTATGGTCTTCTTCTTGGTTTTT

5 MRIIAITEKVIKELFRDKRTLAMMFLAPILIMFLMNVMFSANSNTKVKIGTINV  
 NTKVVSNLNLDNIKHQVRSFKFNSSAKKALKSNKIDALISEDNKSyTVFYANTDS  
 SKTTTLTRQAFKTAVNMTMNSKELISQVKILANKNPKLAQSLQTRSKYIKEKYN  
 GNKNTGFFAKMIPILMGFMVFFLVF

Sequence description:

10 A] Length: 558 bp - 186 aa (partial sequence)  
 B] ATG start codon is preceded by a  
 possible Shine-Dalgarno sequence. Potential  
 leader peptide sequence. C-terminus has yet to be  
 determined.

15

ID-131

20

Clone 3-48

25 GTGATTATCGTTATGAGTAAACATCAAGAAATTTTGGAGTACCTAGAAAAT  
 TTAGCTGTTGGTAAGAGGGTTAGTGTACGCAGTATTTCAAATCATTAA  
 MIIVMSKHQEILEYLENLAVGKRVSRSISNHL

30 Sequence description:

35 A] Length: 100 bp - 33 aa (partial sequence)  
 B] GTG start codon is not preceded by a  
 obvious Shine-Dalgarno sequence. No obvious  
 leader peptide sequence.

40 ID-132

Clone 2-c53

ATGTATAGAGAAATTACCGCTGTCGAACACGATCGCTTTGTGAGCGAATCC  
 AACCAAACAAACCTACTTCAATCTCTTAATTGGCCCAAAGTAAAAGACAA  
 CTGGGGTAGTCAATTACTTGGCTTTTTTTGACGGTGAAACCCAAATTGCCAG  
 CGCTAGTATTCTCATCAAATCACTTCCTCTTGGCTTCTCCATGCTGTATATT  
 5 CCGCGTGGACCAATCATGGATTACTCCAATCTAGATATTGTAAGTAAAGGTC  
 CTTAAGGACCTTAAAGCTTTTGGCAAAAAACAAAGAGCTCTCTTTATCAAG  
 TGTGATCCTCTCATCTATT

10 MYREITAVEHDFVSESNQTNLLQSLNWPVKVDNWGSQLLGFFDGETQIASA  
 SILIKSLPLGFSMLYIPRGPIMDYSNLDIVTKVLKDLKAFGKKQRALFIKCDPLI  
 Y

15 Sequence description:

20 A] Length: 326 bp - 108 aa (partial sequence)  
 B] ATG start codon is preceded by an obvious  
 Shine-Dalgarno sequence. No obvious leader  
 peptide sequence.

25 ID-133

Clone 2-c59

30 ATGGACAAGAAAAAATCTTAGTAACGGGTATTGTGCCTAAAGAAGGTCT  
 AAGAAAGCTTATGGACCGATTTGATGTTACTTATTCAGAAGATCGCCCATT  
 TTCACGTGACTATGTGTTAGAGCATTTATCTGAATATGACGGATGGTTACT  
 CATGGGACAAAAAGGTGATAAAGAGATGATTGATGCAGGTGAAAACCTAC  
 35 AAATTATTTCTTT

MDKKKILVTGIVPKEGLRKLMDRFDVTYSEDRPFSRDYVLEHLSEYDGWLLM  
 GQKGDKEMIDAGENLQIIS

40 Sequence description:

A] Length: 215 bp - 71 aa (partial sequence)



B] ATG start codon is preceded by an obvious Shine-Dalgarno sequence. No obvious leader peptide sequence.

5

ID-134

10

Clone 2-c62

15

ATTTTCGAAAGATGACTACCAAAATATTAGTTTTGGACAGGATCCAGAAGTT  
GTTGATTATGCTGGTCTGTTTGAAAAACGCCGTCCAGTTTTAGAAAAAGCA  
GTTAAAAATTTCTTGCAAGAAGAGAGAGCTACGAGAATGCTATCTGATTTT  
TTGCAAGAAGAAAAATGGGTAAGTATTTGCTGAATTTATGGCGATCAA  
AGAACATTTTGGTAATAAGGCGCTTCAAGAATGGGATGACAAGGCTATTA  
TACGCCGCGAAGAAGAAGCCTTAGCAGGATATCGTCAAAAGCTTAGTGAA  
GTGATAAAATATCATGAAGTAACGCAATATTTCTTTTACAAACAATGGTTT  
GAGTTAAAAGAATATGCTAATGATAAAGGGATTCAAATTATCGGTGATAT  
GCCAATCTACGTTTCTGCCGATAGTGTAGAAGTTTGGACAATGCCTGAACT  
GTTT

20

25

ISKDDYQNIISFGQDPEVVVDYAGLFEKRRPVLEKAVKNFLQEERATRMLSDFLQ  
EEKWVTDFAEFMAIKEHFGNKALQEWDDKAIIRREEEALAGYRQKLSEVIKY  
HEVTQYFFYKQWFELKEYANDKGIQIGDMPYVSADSVEVWTMPPELF

30

A] Length: 459 bp - 153 aa (partial sequence)  
B] More sequencing is required to determine the  
N- and C-termini  
enzyme). - *Streptococcus pneumoniae* (63%)

35

ID-135

Identical to ID-108 described in WO 00/06736

40

Clone 2-c63

ID-136

Clone 2-c66

ATGGCAAAACAGAAAAATAACTGGCGCCGTGTTGGAGTTGGTGTCTTAC  
 5 ACTTGCTTCAGTTGCGACTCTTGCTGCATGTGGAAGTAAATCAGCTTCCCA  
 GGATTCTAATGGAGCGATTAATTGGGCTATTCCAACAGAAATCAATACACT  
 AGATTTATCTAAAGTTACAGACACTTACTCAAATCTAGCTATTGGTAACTC  
 TAGTAGTAATTTCCCTTCGCTTAGATAAAGATGGAAAGACAAGACCAGACTT  
 GGCTACTAAAGTTGATGTTTCAAAAGATGGCTTAACTTATACAGCTACATT  
 10 ACGTAAAGGCTTGAAGTGGTCAGATGGCAGTAAACTTACTGCAAAGGATT  
 TTGTTTATTTCATGGCAACGTTTAGTTGATCCTAAAACAGCTTCACAATATG  
 CTTACCTTGCTGTTGAAGGGCATGTGCTTAATGCCGATAAAATCAACGAAG  
 GACAAGAGAAAGACTTGAATAAGCTAGGTGTTAAGGCAGAAGGCGATGA  
 CAAAGTTGTTATTACTTTATCTAGTCCGTCTCCGCAATTCATCTACTACCTT  
 GCATTCACTAACTTCATGCCACAAAAACAAGAAGTTGTTGAAAAATATGG  
 15 AAAAGATTACGCAACTACTTCAAAAAATACAGTTTACTCAGGACCATATA  
 CTGTTGAAGGTTGGAATGGTTCGAATGGTACTTTCACGCTGAAGAAAAAC  
 AAAAATTATTGGGACGCTAAAAATGTAAAAACAAAAGAAGTTCGCATCCA  
 GACTGTATAAAAAACCAGATACCGCCGTTCAAATGTATAAACGTGGTGAGT  
 TAGATGCAGCTAATATCTCAAATACTTCTGCTATTTATCAAGCTAATAAAA  
 20 ATAATAAGATGTCACAGATGTTCTAGAAGCGACCACTGCCTATATGGAA  
 TATAATACTACTGGTTCTGTGAAAGGGCTTGATAATGTTAAGATTTCGTCGC  
 GCCTTAACTTAGCAACTAACCGTAAAGGAGTTGTTCAAGCAGCCGTTGAT  
 ACAGGCTCAAACCGGCAATTGCTTTTGCACCTACTGGTTTAGCCAAAACA  
 CCAGATGGAAGTGAATTTGGCAAAATATGTTGCCCCAGGTTATGAATATAAT  
 25 AAAACTGAAGCAGCAAAACTCTTTAGACTA

MAKQKNNWRRVGVGVLTLASVATLAACGSKSASQDSNGAINWAIPTEINTLD  
 LSKVTDITYSNLAIGNSSSNFLRLDKDGKTRPDLATKVDVSKDGLTYTATLRKG  
 30 LKWSDGSKLTAKDFVYSWQRLVDPKTASQYAYLAVEGHVLNADKINEGQEK  
 DLNKLGVKAEGDDKVVITLSSPSPQFIYYLAFTNFMPQKQEVVEKYGKDYAT  
 TSKNTVYSGPYTVEGWNGSNGTFTLKKNKNYWDAKNVKTKEVRIQTVKKPD  
 TAVQMYKRGELDAANISNTSAIYQANKNNKDVTVDVLEATTAYMEYNTTGSV  
 KGLDNVKIRRALNLATNRKGVVQAAVDTGSKPAIAFAPTGLAKTPDGTDLAK  
 35 YVAPGYEYNKTEAAKLRL

Sequence description:

- 40
- A] Length: 1143 bp - 381 aa (partial sequence)
  - B] Shine-Dalgarno sequence precedes ATG codon.
  - Possesses a potential leader peptide sequence.

ID-137

Clone 2-c67

5

TTGAGAGTTTATGAAAATAAAGAAGAGTTGAAAAAAGAAATAAGTAAAAC  
ATTTGAGAAATACATTATGGAATTTAATAA  
TATTCCAGAGAATCTAAAAGATAAAAGAATTGATGAAGTTGATAGAACTC  
10 CAGCAGAAAACCTTTCTTATCAGGTTGGCT  
GGACCAACTTGGTTCTTAAATGGGAAGAAGATGAAAGAAAGGGACTTCAA  
GTAAAAACACCATCGGATAAATT

MRVYENKEELKKEISKTFEKYIMEFNNIPENLKDKRIDEVDRTPAENLSYQVG  
15 WTNLVLKWEEDERKGLQVKTPSDKF

Sequence description

20

A] Length: 234 bp - 78 aa (partial sequence)  
B] TTG start codon is preceded by a  
potential Shine-Dalgarno sequence. No obvious  
leader peptide sequence.

25

ID-138

30

Clone 2-c70

ATGTCAAAGTTTGATAGTCAGAAAATAATTACTCCGATTATGAAGTTTGTC  
AATATGCGAGGGATTATTGCACTCAAAGATGGCATGCTAGCAATTTTACCA  
35 CTAACAGTTGTTGGGAGTCTCTTTTAATATTAGGGCAGCTTCCATTT

MSKFDSQKIITPIMK FVNMRGIIALKDGMLAILPLTVVGSFLILGQLPF

40

Sequence description

A] Length: 150 bp - 50 aa (partial sequence)  
B] ATG start codon is preceded by a potential  
Shine-Dalgarno sequence. Possesses a potential

leader peptide sequence.

ID-139

5

Clone 2-c71

10 GAGACCACTTCATCAGTTAAACCAGCAGGAATTGACCGTATCAATCATACC  
TCAACACCCCCGAAGAAAAC TACCCCAACATTGCAACGACGCATAGCTT  
CAAAGATCGTTGTGATACTTTAGAAAGAATTCACAATGAAGACATTGATGT  
TTGTTCTGGATTCATTTGTGGTATGGGAGAGAGCGATGAGGGGCTCATCAC  
ATTAGCTTTCAGACTAAAAGA ACTGAACCCCTATTCTATCCCTGTCAATTTT  
15 TTACTTGCTGTTGAAGGAACACCTCTTGGAATAATACTATTTGACTCCC  
ATTAAATGCTTAAAAATTATGGCCATGTTGCGTTTTGTTTTCTTTCAAGG  
AATTAAGATTAAGTGCTGGACGGGAGGTCCATTTTGAGAATTTTGAATCAT  
TAGTCACCTTACTTGTTGACTCAACTTTTTTGGGAAATTACCTAACAGAGG  
GGGGTCGCAATCAACATACCGATATTGAATTCTTGGAATAATTACAATA  
20 AATCATACTAAAAAGGAATTAATTT

ETTSSVKPAGIDRINHTSTPPKKTPNIATTHSFKDRCDTLERIHNEIDVCSGFI  
CGMGESDEGLITLAFRLKELNPYSIPVNFLLA VEGTPLGKYNYLTPIKCLKIMA  
MLRFVFPFKELRLSAGREVFHFENFESLVTL LVDSTFLGNYLTEGGRNQHTDIEF  
25 LEKLQLNHTKKELI

Sequence description:

30

A] Length: 535 bp - 178 aa (partial sequence)  
B] N- and C-termini require verification

35

ID-140

Clone 2-c73

40

ATGCCGGTTTGGACTGCACAGTCTATTCCAAAGGCATTTT TAGAAAAGCAT  
AATACTAAGGAAGGCACCTGGGCAAACTAACCATTCTAAGTGGTTCTTTA  
GTATTTTACCAGTTATCTCCTGATGGAGAGGAAATCTCGCGGCATATTTT

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### Clone 2c76

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MTKQIIAWAEDEDHLIGVNGGLPWRLPKELHHFKETTMGQALLMGRKTFDG  
MNRRLVLPGRETIILTKDEQFQADGVTVLNSVEQVIKWFQEHNKTLFIVGGASI  
YKAFLPYCEAIKTKVHGKFKGDTYFPDVLNSEF

Sequence description:

- 5 A] Length: 417 bp - 139 aa (partial sequence)  
B] ATG start codon is preceded by a Shine-Dalgarno sequence. No leader peptide sequence

10 ID-142

Clone 2-c78

15 TTGTGGCCAAACTGTGCCCCGCTTATTAATAGCACTTTGTTTCACCATTGAA  
GATATCTTAACATCAGGTGCTCATAGCAACCCTATTTTAATGGGGGTTATA  
CTTGGCGGGACAATTGTAGTAGTGGCGACAGCACCACCTTTCTTCTATGGCA  
20 TTGACAGCTATGCTAGGATTAACCGGAATGCCTATGGCTATAGGAGCCTTG  
TCTGTCTTTGGTTCGTCATTTATGAATGGTGTACTTTTCCATAAATTAAAAC  
TTGGAAGTCGTAAAGATAATATAGCTTTTGCTGTTGAGCCTCTAACTCAAG  
CTGACGTGACTTCAGCTAACCCTATTCCAATCTATGTCACTAATTTTGTTGG  
TGGTGCAGCTTGTGGTATTTTAATTGCCTTGATGAAATTAGTTAATGATACT  
25 CCTGGAACAGCGACACCAATTGCAGGATTTGCTGTCATGTTTGCCTATAAC  
CCAATGATAAAAGTACTAATAACCGCTCTAGGTTGTATTATCCTATCTTTA  
CTAGCAGGCTATTTTGGAGGCATTGTTTTT

MWPNCAPLINSTLFTIEDILTSGAHSNPILMGVILGGTIVVVATAPLSSMALTA  
MLGLTGMPMAIGALSVFGSSFMNGVLFHKLKLGSRKDNIAFAVEPLTQADV  
30 SANPIPIYVTNFVGGAACGILIALMKLVNDTPGTATPIAGFAVMFAYNPMIKVL  
ITALGCIILSLLAGYFGGIVF

Sequence description:

- 35 A] Length: 540 bp - 180 aa (partial sequence)  
B] N- and C-termini have yet to be elucidated

40

ID-143

ID-145

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Clone 3-86

10 ATGTCATATTTTAGAAATTACTGGTATCGTTTTGGAGCAATTTTATTTATTA  
TTTTAGCAGTAATATTGCTTGTTTTTAGACCTGACTGGTCAATGCTTCACTA  
TCTATTGTATTTTTACTTTATGGCACTTCTAGCGCATCAATTTGAAGAATAT  
CAGTTTCCCGGTGGGGCATCACCTATCATTA ACTATGTTGTTTATGATGAA  
GAAGAGCTGATGGATTGTTTTCCAGGCAATACTCAGTCTATTATGTTGGTT  
AATACTATTGCTTGTTTGCTTTACATTGCTAGTATTGCTTTTCCTCAAGCTT  
15 ATTGGCTTGGATTAGGAGTCATGTTCTTTAGTCTAACGCAGCTCTTGGGTC  
ATGGTTTTTCAGATGAATATTA AACTTAA AACTTGGTATAATCCTGGTCTAG  
CAACGACAGTATTTCTCCTAGTACCAATAGCTTGCGCATACATCTATCAAG  
CTAGTGCAGAAGGAATGCTCACTTGGGGAGATTGGCTAGGTGGTTTTATCA  
TGTTGATTGTCTGTGTACTA ACTAGCATTATTGCACCTGTACAGCTATTGAA  
20 GGATAAGGAGACCAATTATATTATTAGTCCTTGGCAAATGGACCGTTTTCA  
TAAGGTCGTTAATTTTGTAAGGATAAAAAATAA

25 MSYFRNYWYRFGAILFIILAVILLVFRPDWSMLHYLLYFYFMALLAHQFEEYQ  
FPGGASPIINYVVYDEEELMDCFPGNTQSIMLVNTIAWLLYIASIAFPQAYWLG  
LGVMFFSLTQLLGHGFQMNIKLKTWYNPGLATTVFLLVPIACAYIYQASAEG  
MLTWGDWLGGFIMLIVCVLTSIIAPVQLLKDKETNYIISPWQMDRFHKVVNFV  
RIKK\*

30 Sequence description:

35 A] Length: 651 bp - 219 aa (full length gene)  
B] Putative ATG start codon is preceded by a  
typical Shine-Dalgarno sequence. Possesses a  
potential leader peptide sequence.

40 ID-146

Clone 3-c88

## Clone 2-c80

5 ATGTTTTTAAGTATAATGGCAGGTGTCATAGCATTGTCTGACAGTTATT  
GCCATTCCACGCTTCATTAAGTTTTACCAATTGAAGAAAATTGGCGGGCAA  
CAAATGCATGAAGATGTCAAACAACATCTAGCCAAAGCAGGTACGCCGAC  
AATGGGAGGAACGGTATTTT

10 MFLSIMAGVIAFVLTVIAIPRFIKFYQLKKIGGQQMHEDVKQHLAKAGTPTMG  
GTVF

## Sequence description:

15 A] Length: 172 bp - 57 aa (partial sequence)  
B] Shine Dalgarno sequence precedes 'ATG' start  
codon. Possesses a potential leader peptide  
sequence.

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## ID-144

25

## Clone 3-83

30 ATGAAACCATATTTATCTTTTATTGGTAGAACGTTATTATACTTCGGTATTT  
TATTGTTACTAATTTACTTTTTTGCATACCTTGGTCGCGGACAAGGCAGTTT  
TATTTATAA

MKPYLSFIGRTLTYFGILLLLIYFFAYLGRGQGSFIY

35

## Sequence description:

40 A] Length: 113 bp - 37 aa (partial sequence)  
B] Putative ATG start codon is preceded by a  
typical Shine-Dalgarno sequence. Possesses a  
potential leader peptide sequence.  
This orf is not in frame with nuc



ATGCCACTTACAGCACTTGAAATTAAAGATAAAACATTTTCATCAAAATTT  
CGCGGTTATAGCGAAGAAGAAGTT

5 MPLTALEIKDKTFSSKFRGYSEEEV

Sequence description:

10

A] Length: 75 bp - 25 aa (partial sequence)  
B] Putative ATG start codon is preceded by a  
typical Shine-Dalgarno sequence. No leader  
peptide

15

ID-147

20 Clone 3-90

ATGTCACCTTTTTCAAGAAAAAATTGCTTACAATTGCGCTAAAAAGGAAGCG  
CTTTATAAAGAGAGTTTAGGACGCTACGCCTTGAGATCAATGCTAGCAGG  
25 GGCTTATTTGACAATGAGTACTGCTGCCGGTATCGTCGCAGCTGATACTAT  
TGGTAAAATTTCTCCTGCTCTATCAGGTTTTGTATTTGCTTTTCATCTTTAGTT  
TTGGACTTATTTATGTTTTAATATTTAATGGTGAATTGGCGACATCTAATAT  
GCTTTATCTCACTGCAGGAGCCTATAATAAAAATATCTCTTGGAAAAAAGC  
CATAACAATTTTAATTTATTGTACTTTTTTCAACCTCGTTGGTGCTTGTATA  
30 TTAGCTTGGTTGTTTAA

MSLFQEKIAYNCAKKEALYKESLGRYALRSMLAGAYLTMSTAAGIVAADTIG  
KISPALSGFVFAFIFSFLIYVLIFNGELATSNMLYLTAGAYNKNISWKKAITILI  
YCTFFNLVGACILAWLF

35

Sequence description

40

A] Length: 406 bp - 125 aa (partial sequence)  
B] Putative ATG start codon is preceded by a  
typical Shine-Dalgarno sequence. Possible  
leader peptide

Clone 3-92

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Clone 3-94

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ATCCACCAACCAATGGGCGGAACAGGCGGAGGTACACAGCAATCTGATAT  
 GGCTATCGCTGCTGAGCATCTTTTAAAAACGCGTCATACTTTAGAAAAAAT  
 CTTAGCTGATAATTCTGGTCAATCTATTGAAAAAGTCCATGATGATGCAGA  
 GCGTGATCGTTGGATGAGTGCTCAAGAACAATTGATTATGGCTTTATTGAT  
 5 GCTATTATGGAAAATAATAATTTACAATAATAGATTTAAAAGAGTTGAGTT  
 TACCAACTCTTTTTTTTATTTGTTGGAATTATGTTATAATCTTAGTAATTACA  
 GATATGACGCAGAAAGGAAAAAATTATTGA

MIPVVIEQTSRGERSYDIYSRLLKDRIIMLTGQVEDNMANSIIAQLLFLDAQDN  
 10 TKDIYLYVNTPGGSVSAGLAIVDTMNFIKSDVQTIVMGMAASMGTHASSGAK  
 GKRFMLPNAEYMIHQPMGGTGGGTQQSDMAIAAEHLLKTRHTLEKILADNSG  
 QSIEKVHDDAERDRWMSAQEHLIMALLMLLWKIIYNNRFRVEFTNSFFICW  
 NYVILVITDMTQKGKNY\*

15

Sequence description

20

A] Length: 693 bp - 231 aa (full length gene)  
 B] Putative ATG start codon is preceded by a  
 typical Shine-Dalgarno sequence. No leader  
 peptide. Significantly, it would appear to have a  
 very hydrophobic C-terminus.

25

ID-150

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Clone 2-c86

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ATGAAACCAAAAaTTATTGGTGTACTTGGTCTAGGAATATTTGGACAAACA  
 CTCGCACAAGAATAAGTAACCTTTGAACAAGATGTTATTGCTATTGACAGC  
 AATCCTGAAAATGTACAAGCTGTCGCCGAAGT  
 TGTTACAAAAGCAGCTATCGGAGACATTACTGATTTAGCTTTCCTAAAACA  
 CATCGGGATCAGTGACTGTGATACTGTTATTATTGCTACAGGAAACAGTTT  
 AGAGAGCTCAGTATTGGCCGTAATGCACTGTAAAAAGTTAGGCGTCCCAC  
 AAGTTATTGCTAAAGCTCGAAACCTTGTATACGAAGAAGTACTTTATGAAA  
 TTGGTGCTGATTTGGTTATCTCTCCGGAGCGAGAATCTGGGCAAAATGTTG  
 CTGCAAACCTCATGAGAAATAAAATTACAGATGTCTTCCAGATTGAATCTG  
 ATATTTCTGTCATTGAATTT

MKPKIIGVLGLGIFGQTLAQELSNFEQDVIAIDSNPENVAEAVVTKAAIGDI  
 TDLAFLKHIGISDCDTVIIATGNSLE

SSVLAVMHCKKLGVPQVIAKARNLVYEEVLYEIGADLVISPERESGQNVAAN  
LMRNKITDVFQIESDISVIEF

5      Sequence description:

10 A] Length: 459 bp - 153 aa (partial sequence)  
B] Putative ATG start codon is preceded by a  
typical Shine-Dalgarno sequence. Possesses a  
potential leader peptide sequence.  
This orf is not in frame with nuc

15 ID-151

20 Clone 2-c88

25 GTGCGTTATAGTAAAGAGATTATTCAGTTAGCTATACCAGCTATGATTGAA  
AATATCTTACAAATGCTCATGGGAGTAGTTGATAATTATCTAGTGGCTCAG  
TTAGGTGTTGTAGCAGTATCAGGTGTTTCAGTTGCTAATAATAATTACT  
ATTTATCAAGCTATTTTTATAGCTTTAGGGGCGAGTATAGCAAGTCTATTG  
GCCAAGTCGTTAGCAGGTAGTGAGAAGGATGATGCAATTTTCAGTATGTTCT  
CAAGCCATTTTTCTAACATCACTGATAGGGGCGAGTATTAGGAATTATCTCG  
ATTGTTTTTGGACAACTTTCTTT

30 MRYSKELQLAIPAMIENILQMLMGVVDNYLVAQLGVVAVSGVSVANNIITIY  
QAIFIALGASIASLLAKSLAGSEKDDAISVCSQAIFLTSLIGAVLGIISIVFGOTFF

35 Sequence description

40 A] Length: 330 bp - 110 aa (partial sequence)  
B] Putative GTG start codon is preceded by a  
typical Shine-Dalgarno sequence. May have a  
leader peptide

ID-152

## Clone 2-c92

5

TTGATTAACAAGTATTCGTGCTTTTTGAAGAGGATTCTCCATAATAATACT  
CCTTTAATAGTTATCGTGAGAAGTATTTTAAAGAAAAACCGCCAAGGTAG  
AGCGACATTTCTGCCTTTAACTACAATAAAACCAAGAGAATTAGCACAAAC  
ATTATCTCTCAAAATTACAAAGTTCTCAAGGGTTTTTAGGAATAGCTAGTG  
AATTGGTAACCTATGATCAACGCTTGTCAAACATTTTT

10

MINKYSCFLKRILHNNTPLIVIVRSILKKNRQGRATFLPLTTIKPRELAQHLYLSK  
LQSSQGFLGIASELVTYDQRLSNIF

15

Sequence description

A] Length: 240 bp - 80 aa (partial sequence)

B] No obvious Shine Dalgarno sequence precedes the Putative TTG start  
codon

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ID-153

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## Clone 2-c94

30

TTGTTGACTCACAAAAATATATTATTAACCATTATATTTGGATTATTTATGA  
TTATATTATCAGCATGTGGTATGTCTAATAAGGAAATGGCTGGTATTGATA  
ATTGGGAACATTATCAAAAGGAAAAGAAAATTACTATTGGATTTGATAAT  
ACTTTTGTTCCCTATGGGATTTGAAAGTCGTTCTGGTGACTATACCGGCTTTG  
ATATTGATTTAGCTAATGCTGTTTTTAAAGAATACGGTATTTCAAGTGAAAT  
GGCAGCCTATTAACCTGGGATATGAAAGAACTGAACTTAATAATGGTAAT  
ATAGACCTTATTTGGAATGGTTATTCAAAAACGGCAGAACGTGCTAAAAA  
AGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTGTTACTAA  
AACTTCATCACATATTAATAGTATTAAGGATATGAAGGGGAAAAAACTAG  
GAGCCCAGTCGGGTTTCATCTGGTTTTGATGCTTTTAACGCTAAACCTGATA  
TTTTAAAAAAGTTTGTAAGGAAAAGAAGCAGTTCAATACGATACTTTC  
ACTCAGGCTTTGATTGATTTAAAAAATAACCGTATTGATGGTCTTTTGATT  
GATGAAGTTTATGCTAACTATTATTTAAAGCAAGAAGGAA

35

40

MLTHKNILLTIIFGLFMIILSACGMSNKEMAGIDNWEHYQKEKKITIGFDNTFV  
PMGFESRSGDYTGFDIDLANAVFKEYGISVKWQPINWDMKETELNNGNIDLI  
WNGYSKTAERAKKVAFTNPYMNNHQVIVTKTSSHINSIKDMKGKKLGAQSG  
SSGFDAFNAKPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANY  
5 YLKQEG

Sequence description

10 A] Length: 649 bp - 216 aa (partial sequence)  
B] TTG start codon is preceded by a possible  
typical Shine-Dalgarno sequence. Has a  
leader peptide

15

ID-154

20

Clone 2-c100

25 ATGAAAATTTGGAAAAAATAACCTTAATGTTTTCTGCAATTATTTTAACA  
ACAGTAATTGCATTGGGAGTCTATGTTGCCTCAGCTTATAATTTTTCGACTA  
ATGAATTGTCTAAGACTTTT

MKIWKKITLMFSAIILTTVIALGVYVASAYNFSTNELSKTF

30

Sequence description

35 A] Length: 123 bp - 41 aa (partial sequence)  
B] ATG start codon is preceded by a potential  
typical Shine-Dalgarno sequence. Has a  
typical leader peptide

40

ID-155

Clone 2-c1

ATGAAAAAACAAAGACTATTACTGCTTTTTGGAGGCTTATTAATAATGATA  
5 ATGATGACAGCATGTAAGGATTCAAAAATCCCAGAAAACCGCACGAAAAA  
GGAATACCAGGCAGAACAGAAATTTTAAGTCATACTTTAAATATATATCAG  
ATAAAAATAACTATTTAGATAATATAAAAAGTTTATTACTTTTCTATAAGTA  
TTTCTAAAGATGTACAAGATAAAGTCAGTGAAACAACAACCTTGTTTCATATA  
GACTAGAAAAGCAAAAGAATCAAGAGTTCATTGGTAATTTTGAACATGAA  
GTTAGTGAATCTAGTCAATATTCAACCGAAGTTAAAAATCAAATACAGTAT  
10 CCAATCCAGTATAAAGATAATTCAATTCGTTTTACTGAAAAAACACCGTCA  
GAACGTTATGATGAGTTTGTGTTTTAGTTCATTGATTCTTCATTATTA  
AATATAAAATATATGATTACTTACTAAAACATCCCGAAACTGAATTA  
GGTGTTCCTATAAGATTCCTATAAATTCTGAAATTGTAGCCCCCTTTTATAA  
ATCAATTAAATATAAAAAATCCTAAAAAATCATCTATTTTCGGTTACAAAAA  
15 CGGAAAGTAAAGAATATTATTATACAATCAGTATTGATACTGATTCTGAGA  
TATATTCTATATTCGAAGGTATTCAT

MKKQRLLLLFGGLLIMIMMTACKDSKIPENRTKKEYQAEQNFKSYFKYISDKN  
20 NYLDNIKVYYFSISISKDVQDKVSETTTCYSRLEKQKNQEFIGNFEHEVSESSQ  
YSTEVKNQIQYPIQYKDNSIRFTEKTPSERYDEFVFSSFDSSLLKKYKIYDYLLK  
HPETELKGVSYKIPINSEIVAPFINQLNIKNPKKSSISVTKTESKEYYYTISIDTDS  
EIYSIFEGIH

25 Sequence description

30 A] Length: 687 bp - 229 aa (partial sequence)  
B] ATG start codon is preceded by a potential  
typical Shine-Dalgarno sequence. Has a  
typical leader peptide. C-terminus has yet to be  
verified

35 ID-156

Clone 2-c5

40 ATGACATTTGACACCATTGATCAATTAGCGGTTAATACAGTCCGCACGCTT  
TCTATTGATGCTATCCAAGCAGCAAATTCTGGGCACCCAGGTCTTCCTATG  
GGAGCTGCGCCTATGGCTTATGTGCTTTGGAATAAATTCTTAAATGTAAAC  
CCAAAAACAAGTCGCAATTGGACAAACCGTGACCGTTTTGTACTTTCAGCT

GGGCATGGTTCAGCTCTTCTTTATAGCCTACTTCATTTAGCTGGCTATGATT  
TATCAATTGATGATTT

5 MTFDTIDQLAVNTVRTLSIDAIQAANS~~GHPGLPMGAAPMAYVLWNKFLNVNP~~  
KTSRNWTNRDRFVLSAGHGSALLYSLHLAGYDLSIDD

Sequence description

10

A] Length: 272 bp - 90 aa (partial sequence)  
B] ATG start codon is preceded by a potential  
typical Shine-Dalgarno sequence. No obvious  
leader peptide

15

ID-157

20

Clone 2-c8

25 ATGAGAACACTATTTAGAATGATATTTGCTATTCCAAAGTTTATCTTTAGA  
TTGATTTGGAATATCATTTGGGGAATATTCAAGACAGTTCTTGTTATTGCG  
ATTATTTTATTTGGCTTGTATTACTATGCGAATCACAGTCAATCAGAATTTG  
CTAATCAACTTAGTGACATTATTCAGACAGGAAAAACATTTT

30 MRTLFRMIFAIPKFIFRLIWNIIWGIFKTVLVIAIILFGLYYYANHSQSEFANQLS  
DIIQTGKTF

Sequence description

35

A] Length: 197 bp - 65 aa (partial sequence)  
B] ATG start codon is preceded by a potential  
typical Shine-Dalgarno sequence. Possesses a  
leader peptide

40

ID-158



## Clone 2-c9

5

ATGTCAAAAAAAAAATAATATTAGGAATTTTATCTCTTTTATCTGTCGTTACTT  
TGGTGGCGTGTGGTTCATCAGACAAACAGCTACAAGATAAAGTTGAGAAA  
AAAGGGAAGTTAGTTTTAGCGGTGAGTCCAGATTATGCTCCCTTTGAGTTT

10

MSKKIILGILSLLSVVTLVACGSSDKQLQDKVEKKGKLVLA VSPDYAPFEF

## Sequence description

15

A] Length: 153 bp - 51 aa (partial sequence)  
B] ATG start codon is preceded by a potential  
typical Shine-Dalgarno sequence. Possesses a  
leader peptide (not in frame with nuc)

20

ID-159

25

Clone 2-c10

ATGAAAAATCAAAGACTATTACTGCTTTTTGGAGGCTTATTAATAATGATA  
ATGATGACAGCATGTAAGGATTCAAAAATCCCAGAAAACCGCACGAAAAA  
30 GGAATACCAGGCAGAACAGAATTTTAAGTCATACTTT

MKNQRLLLLFGGLLIMIMMTACKDSKIPENRTKKEYQAEQNFKSYF

35

## Sequence description

40

A] Length: 139 bp - 46 aa (partial sequence)  
B] ATG start codon is preceded by a potential  
typical Shine-Dalgarno sequence. Possesses a  
leader peptide

ID-160

Clone 2-c11

5

ATGATTGGAAAATTATATTATAGCTATAGAAAGTCACGCTTATTAAGAAGT  
ATTTTATGGCTTATTTTAATTGTTGGTGTATATATGTTAGGACAACGTGTTT  
TATTATCCACTGTTTCCTTTATCACATCAAGAGATAAACTAGCAGTAGATC  
10 AACATTTACTCAATAACTTTTCAGCAGTAAGTGGTGGGAGTTTTTAATAAAT  
TAAATGTTTTCACACTGGGGTTGAGTCCATGGATGTCAAGTATGATTATTT  
GGAGATTTCGTTTCCTTATTTTCGTGGGCAAAAAATGCAACGAAGCGAAAA  
GCAGAAGTAGCTCAATATACTTTAATGCTTACTATCTCAGTTATACAAGCA  
TATGGTGTTTCAGGAAATCAATTTATAAAAAGCTCTTTATTAGGTTCTTATA  
15 GTGATATTGTTTTT

MIGKLYYSYRKSRLRLSILWLILIVGVYMLGQRVLLSTVPLSHQEIKLAVDQHL  
LNNFSAVSGGSFNKLVFTLGLSPWMSSMIIWRFVSLFSWAKNATKRKA EVA  
QYTLMLTISVIQAYGVSGNQFIKSSLLGSYSDIVF  
20

Sequence description

25

A] Length: 423 bp - 141 aa (partial sequence)  
B] ATG start codon is preceded by a potential  
typical Shine-Dalgarno sequence. Possesses a  
leader peptide

30

ID-161

35

Clone 2-c13

ATGAAAGGTCTATTGGATTTTTTTAGTTAATATTGCCAGAACGCCAGCTATT  
TtagTCGCCTTGATAGCCATTATCGGTTTtagTACTGCAGAAAAAAGGTGTT  
40 CCTGATATTGTAAAAGGTGGAATAAAAAACATTTGTTGGCTTCTTAGTGGTT  
TCTGAAGGTGCAGGGATAGTCCAAAATTCCTTGAATCCATTTGGAAAAATG  
TTTGAACATGCTTTTCATTTGGTGGGGGTAGTTCCTAATAATGAAGCCATT  
GTAGCAGTAGCTCTTACGAAGTATGGCTCAGCAACTGCTTTGATTATGTTA  
GCGGGAATGATTTTTAATATTTTAATTGCTCGTTTTACAAA

MKGLLDFLVNIARTPAILVALIAIIGLVVLQKKGVDPDIVKGGIKTFVGFLVVSEG  
AGIVQNSLNPFGKMFEHAFHLVGVVPNNEAIVAVALTKEYGSATALIMLAGMI  
FNILIARFTK

5

#### Sequence description

- 10                   A] Length: 348 bp - 116 aa (partial sequence)  
                    B] ATG start codon is preceded by a potential  
                    Shine-Dalgarno sequence. Possible leader  
                    peptide

15

ID-162

Clone 2-c21

20

TTGGTTGGTAAGCCCCAATTACTATTTTTAGATGAACCTACTTCCGGAATG  
GATACTTCCACACGTCAACGATTTTGGAAGCTGGTTGCGACACTAAAAAA  
AGAAGGTGACACAATTGTCTATTCTAGTCATTATATCGAAGAGGTTAGAAC  
25                   ATACAGCTGATAGGATTTTAGTACTTCATAAAGGAAAGTTATTACGCGATA  
                    CAACCCCTTTGCCATGAAGCAAGAAAAAACCGAAAAGTTATTCACCGTT  
                    CCGCTTAGTTATCAAAAATTATTACCTACCTATTTGATTACAGAGTGTGAA  
                    GCCAAGAGTGATAGTATAACGTTTGTTACTGGGGAGGCTGAAACTGTATG  
                    GAAAATACTGGCAGATAATGGTTGTCCTATTGAAGCTATTGAGATGACCA  
30                   ATAGAACTTTGTAAATCGTATTTTTGAGACTACTAAGGAGGTAAACATG  
                    AGAATCTTTA

35

MVGKPQLLFLDEPTSGMDTSTRQRFWKLVALTKKEGDTIVYSSHYIEEVEHTA  
DRILVLHKGKLLRDTPFAMKQEKTEKLFTVPLSYQKLLPTYLITECEAKSDSI  
TFVTGEAETVWKILADNGCPIEAIEMTNRTLLNRIFETTKEVKHENL

#### Sequence description

40

- A] Length: 462 bp - 155 aa (partial sequence)  
B] B] Putative TTG start codon is not preceded by  
an obvious Shine-Dalgarno sequence. No obvious  
leader peptide. N- and C- termini require further

examination.

ID-163

5

Clone 2-c25

10

TTGAAAAAATCCAAGAGAAGCCGTAAGGCAGTGACAACAAGTGGTGAGA  
AGACTTTACTTGAGGATTTGGCAAAAATGAATTCCTAGACGAAGTCATTA  
ATGTTATGGTTTTATATACCTTGAATAAGACAAAATCTGCTAACTTAAATA  
AGGCCTATATCATGAAAGTTGCTAATGATTTTGCCTTTCAGAATGTTATGA  
CGGCCGAAGATGCTGTGCTTAAAATTCGTGATTTTTCAGATCAAAAAGTAA  
GGACTAAAACAGAAACGAAGAAGAAACAATCGAATGTTCTGAATGGAGT  
15 AATCCTGATTATAAAGATGAGGTTAGCCCAGAAAAAGAAATTGAATTAGA  
ACAGTTT

20

MKKSKRSRKAVTTSGEKTLLEDLAKMNFLDEVINVMVLYTLNKTKSANLNK  
AYIMKVANDFAFQNVMTAEDAVLKIRDFSDQKVRTKTETKKKQSNVPEWSN  
PDYKDEVSPKEIELEQF

Sequence description

25

A] Length:360 bp - 120 aa (partial sequence)  
B] N- and C- termini require verification.

30

ID-164

35

Clone 2-c28

40

ATGACGAATCATATTACTAAACTGATAGAAAATAGCGGAAAAAAATTGAC  
AGAAATTAGCGAAGCTACAGATATAGCCTATCCTACACTTTCTGGATACAA  
TCAAGGAATCCGCAAACCTAAAAAAGATAATGCTGAAAAATTGGCAAAAT  
ACTTTAATGTTTCCGTCGCTTACATTATGGGACTTGATAGCAACCCACATG  
CTCCATCAAATCTT

MTNHITKLIENSGKKLTEISEATDIA YPTLSGYNQGIRKPKKDNAEKLAKYFNV  
SVAYIMGLDSNPHAPSNL

## Sequence description

5

A] Length:218 bp - 72 aa (partial sequence)  
B] ATG start codon is preceded by an  
obvious Shine Dalgarno sequence. No obvious  
leader peptide.

10

ID-165

15

Clone 2-c29

20

TTGATGAAAAGGAATAAACATTTACCGTTAACAGAACTACCTATTATATT  
TTATTAGCTTTGTTTGAGGAAGCGCATGGCTATGCTATTATGAAAAAAGTT  
GAAGAAATGAGTGGCGGTGATGTTAGAATAGCCGCAGGGACAATGTACGG  
TGCCATTGAAAATTTACTTAAACAAAAATGGATAAAGTCTATCTCAAGTGA  
CGATAGAAGAAGAAAAGTTTATATTATTACTGAGACAGGAAAAGAAATAG  
TAGAACTTGAAACGAATCGATTAAAGAAAGTTACTTAATACTGCTAATCAGT  
TGGGTTTTGGAGGAGATGGTTATGATAAAGTTT

25

MMKRNKHLPLTETTYIILLALFEEAHGYAIMKKVEEMSGGDVRIAAGTMYG  
AIENLLKQKWIKSISSDDRRRKVYIITETGKEIVELETNRLRKLLNTANQLGFG  
GDGYDKV

30

## Sequence description

35

A] Length:337 bp - 112 aa (partial sequence)  
B] TTG start codon is preceded by an  
obvious Shine Dalgarno sequence. Actual start  
codon may ATG that comes immediately after the  
TTG. Potential leader peptide.

40

ID-166

## Clone 2-c35

5 CCCATTACTGGTGAGTTAATAGCTGAGAAATTAGGAGTACCAAGAGCAGC  
ACTAAGGTCTGATTTGCGGGTTTTAAGTATGCTAGGTATCATAGATGCAAA  
ACCTAAGGTTGGTTATTTTTATTTAGGACAGTATCATGCTTCAATAGGGAC  
AAGTCATTTTGAAAAGATGACAGTTTCAGAAATTATGGGGATCCTTCTGAC  
AGTTCATCAAAAAGATTTCAGTTTATGATGTTATTGTACATATTTTTATGGA  
10 AGATGCTGGTTGTGCTTTTATCTTGGATGATGATGATTTTCTCTGTGGAGTC  
GTGTCACGTAAAGATTTACTAAAAACCAGTATTGGCGGAGGAGATCTTTCT  
AAAATGCCAATAGGAATGGTGATGACACGTATGCCACACGTGACAACCTGT  
TTTAGAAAATGAAAGTCTTTTTGCGGCAGCTGATAAATTAGTGAGCAGAA  
AAGTGGATAGTCTCCCTGTCGTTTCGTCATGATAAGCAATATCCCGAAAAAT  
15 TTA

PITGELIAEKLGVPRALRSDLRVLSMLGIIDAKPKVGYFYLGQYHASIGTSHF  
EKMTVSEIMGILLTVHQKDSVYDVIVHIFMEDAGCAFILDDDDFLCGVVSRKD  
LLKTSIGGGDLSKMPIGMVMTRMPHVTTVLENESLFAAADKLVSARKVDSL PV  
20 VRHDKQYPEKF

## Sequence description

25 A] Length:511 bp - 170 aa (partial sequence)  
B] N- and C-termini to be determined

30 ID-167

## Clone 2-44

35 TTGGAAGTCATCATGCAATTTATTTATAGTATTATTGGTATTTTATTGGTAT  
TAGGAATTGTGTATGCAATTTCTTTCAATCGTAAGAGTGTTTCTCTAAGTTT  
AATTGGAAAAGCTCTTATCGTTCAATTCATTATTGCGCTAATCTTAGTACGT  
40 ATCCCACTAGGCCAACAAGTTGTTAGTGTTGTTTCAACTGGAGTTACTAAA  
GTAATCAACTGTGGTCAAGCTGGTTT

MEVIMQFIYSIIGILLVLGIVYAISFNKRKSVLSLIGKALIVQFIILVRIPLGQQ  
VVSVVSTGVTKVINCGQAG

## Sequence description

5

A] Length:233 bp - 77 aa (partial sequence)  
B] TTG start codon is preceded by a  
possible Shine Dalgarno sequence. Actual start  
codon may occur further downstream. Potential  
leader peptide.

10

ID-168

Clone 2-46

15

CAACCTAATAAAGCTTTAGAAAGTGATGAGATTGATATTAATGCTTTCCAG  
CATTATAATTACTTAACCAATTGGAATAAAGCAAATAAGACCAATCTTGTT  
TCCGTTGCTGAGACATACTTTACTTCCTTTAGATTATACTCTGGTACTAAGA  
ACGGTAAAGGTAAATACCAAACAGTTTCTGAAATTCCAAATAAAGCAACT  
ATTACTATCCCAAACGATGCAGTTAACGAAAGTCGCTCTCTCTACTTGTTA  
CAATCAGCAGGCTTGCTAAAATTGAAAGTATCAGGTGATACATTAGCAAC  
AATGTCAGATGTTGTTTCCAATCCTAAATCTTTAGATT

20

25

QPNKALESDEIDINAFQHYNYLTNWNKANKTNLVSVAETYFTSFRLYSGTKN  
GKGKYQTVSEIPNKATITIPNDVNESRSLYLLQSAGLLKLKVSGDTLATMSD  
VVSNNPKSLD

30

Sequence description

A] Length:344 bp - 114 aa (partial sequence)  
B] N- and C- termini require verification

35

ID-169

40

Clone 2-47

ATGAAATGTATAATAAATAATATAAAATAAAATAAAAAATGATAATTGAGAT  
TTATCATAGAAGGAAAACCTATTTTGAAATTAAATAAAATCATATTATCTAC

TGCAGCTCTTACTGCTCTCTTTTTAGGATATAATAGCGTTACTGCGGATACA  
TATAATAACTATCAGCCACATAGATCAAATAATATGGATTTAACTGAGGA  
ATATAACTATAATAACCAGATAGAACTTCAGGAGCGTATAAAAAACCTAA  
ATATACCTTTT

5

MKCIINNINKIKMIEIYHRRKTILKLNKIILSTAALTALFLGYNSVTADTYNNY  
QPHRSNNMDLTEEYNNNQIELQERIKNLNIPF

10

Sequence description

15

A] Length:264 bp - 88 aa (partial sequence)  
B] There is a Shine-Dalgarno sequence upstream  
of this sequence. Potential leader peptide  
sequence

20

ID-169

Clone 2-47

25

ATGAAATGTATAATAAATAATATAAAATAAAAAATGATAATTGAGAT  
TTATCATAGAAGGAAAACCTATTTTGAAATTAAATAAAATCATATTATCTAC  
TGCAGCTCTTACTGCTCTCTTTTTAGGATATAATAGCGTTACTGCGGATACA  
TATAATAACTATCAGCCACATAGATCAAATAATATGGATTTAACTGAGGA  
ATATAACTATAATAACCAGATAGAACTTCAGGAGCGTATAAAAAACCTAA  
ATATACCTTTT

30

MKCIINNINKIKMIEIYHRRKTILKLNKIILSTAALTALFLGYNSVTADTYNNY  
QPHRSNNMDLTEEYNNNQIELQERIKNLNIPF

35

Sequence description

40

A] Length:264 bp - 88 aa (partial sequence)  
B] There is a Shine-Dalgarno sequence upstream  
of this sequence. Potential leader peptide  
sequence



ID-170

5 Clone RS-58b

TTGGGTGATTATTATGGTAAGAAATATTTTGGTGAGGCAGCTAAAAAAGA  
CGTCGAACATATGGCTAAGAAAATCATTAATGTCTATAAAACACGGTTAA  
10 AAAACAACACTTGGTTATC  
AGAAAATACAAAAGCAATGGCCATTAAGAAACTTGATAACATGAGATTAA  
TGATTGGCTATCCAGAAGATTATCCTGATCTTTATCGTCAGTACCAATTTG  
ATAGTAAAGCAAGCTTCTTTGAAAACAATGATAACTACAGAAAATTATCG  
AACAAGAAAACATTTGAAGAATTTAACCAGTCTAATCAACGTGAACATTG  
15 GCAAATGAGTGCCAATGCTGTAAATGCTTATAATGATCCTAATACCAATTC  
CATAGTCTTTCCAGCAGCGATTTTTCAATCACCAGTGTACGATAAACTAA  
AACAGTTAGTCAAAATTATGGAGCTATCGGAGCAATTATTGGTCATGAAAT  
TTCACACTCATTTGATATTAATGGTATGAAATATGACGAGAAAGGGAATCT  
TCACGATTGGTGGACTAAAGAAGATTTAAATCATTATAAGAAATCAACAC  
20 AAGCTATGATTGACCAATGGGATGGCCTTAAAGCAGATGGCGGTAAAGTT  
GATGGTAAATTAACCTTTAGCAGAAAATATTGCAGATAATGGTGGTGTATG  
GCATCTCTAGAAGCTCTTAAGACTGAAAAAATCCAACTATAAAGAATTTT  
TTGAATCATGGGCAAGTATTTGGCGTCAAAAAGCAACCAAAGAACAAGT  
AAGTCCTCAATTCAGTCAGATGTTTCATGCACCATATGAATTGA >  
25 GAGCTAACATCCCAGTACGTAATTTCCAAGAATTTTATGATGCCTTTGGTG  
TTAAAAAAGGCGATTCAATGTATCTAAAACCAGAAAAACGTTTGACACTTT  
GGTAA

30 MGDYYGKKYFGGEAAKKDVEHMAKKIINVYKTRLKNNTWLSENTKAMAIIKK  
LDNMRLMIGYPDYPDLRQYQFDSKASFFENNDNYRKLSNKKTFEEFNQSNQ  
REHWQMSANAVNAYNDPNTNSIVFPAAIFQSPLYDKTKTVSQNYGAIGAIIGH  
EISHSFDINGMKYDEKGNLHDWWTKEDLNHYKKSTQAMIDQWDGLKADGG  
KVDGKLTLAENIADNGGVMASLEALKTEKIQTIKNFLNHGQVFGVKKQPKNK  
35 VSPQFSQMFMHHMN\*

Sequence description:

40 A] Length: 819 bp - 272 aa (full length gene)  
(107 bp of additional DNA sequence (> onwards) is  
also included. While not in-frame with the  
described orf, it also shares strong homology  
with the neutral peptidases.

5

10

Clone 2-18/22b (Mod2)

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ID-172

5

Clone 2-54balternate (107b)

10 TTGAAAAAAATTATTACTTCTATTCTATTACTTAGTTGCATTTTTTTTATGC  
CAACCATCTCTGCTGAATCTTTTAATGCTTCCGCTAAACATGCCTTAGCAGT  
TGATTTAGATTCAGGAAAAATCTTGTATGAAAAAGATGCTAACAAACCCG  
CTGCTATTGCTTCCTTGACTAAAATAATGACCGTTTATATGGTCTATAAAG  
AAATTGATAACGGTAACCTCAAGTGAATACCAAAGTAAATATATCTGAC  
TACCCTTATCAACTAACACGCGAATCTGATGCTAGTAATGTTCCTTTAGAA  
15 AAAAGGCGCTATACTGTAAACAACCTCGTGGACGCTGCCATGATTTCTAGT  
GCTAACAGTGCAGCCATTGCTTTAGCTGAACATATTTTCAGGAACTGAAAGT  
AAATTTGTTGATAAAATGACTGCTCAATTGGAAAAGTGGGGAATTCATGAT  
AGCCACCTAGTCAATGCTTCTGGCTTAAATAATAGTATGTTAGGCAATCAC  
ATTTATCCAAAATCGTCACAAAACGACGAAAATAAAATGAGTGCACGTGA  
20 TATTGCTATTGCTGCCTACCATTGTTCAACGAATATCCTTCCATTCTTAAG  
ATTACTAGTAAGTCCGTTGCTAAATTTGATAAAGATATTATGCATTCTTAT  
AACTACATGCTACCAGATATGCCTGTCTTTAGACCAGGTATTACAGGTTTG  
AAAAGTGGGACAACGGAATTAGCTGGCCAATCTTTTATTGCTACATCTACT  
GAAAGTGGGAATGAGACTACTCACTGTTATTATGCATGCTGATAAGGCCGAT  
25 AAAGACAAATATGCTCGCTTTACAGCAACTAACTCTCTCTTGAACATATATC  
ACAAACACCTACGAACCTAACCTTGTATTAGCTAAAGGAGCTGCATATAA  
AGGTAAAGAAGCAAGTGTGAGAGACGGAAAAGAACAATCGGTCATCGCT  
GTTGCTAAAAACGATTTGAAAGTAGTACAGAAGAAAAATATCACTAAACA  
AAATCAGTTAAAAATTAACCTTTAAAAAAGAGCTTACTGCTCCTATTACAAA  
30 AAAAGAGAACCTAGGGAAAGCTTATTACGTTGACCTTAATAAGGTTGGAA  
AAGGCTATCTCATAAAGGAACCTAGCGTTCATTTAGTGGCAAAGATAGT  
ATTGAGCGCAGTTTCTTCCTCAAAGTGTGGTGAATCATTTTGTGCGCTAC  
GTTAACGAAAAACTTTAA

35

40

MKKIITSILLLSCIFFMPTISAESFNASAKHALAVDLDSGKILYEKDANKPAAIA  
SLTKIMTVYMVYKEIDNGNLKWNTKVNISDYPYQLTRESASNVPLEKRRYT  
VKQLVDAAMISSANSAAIALAEHISGTESKFVDKMTAQLEKWGIHDSHLVNA  
SGLNNSMLGNHIYPKSSQNDENKMSARDIAIAAYHLVNEYPSILKITSKSVAKF  
DKDIMHSYNYMLPDMPVFRPGITGLKTGTTELAGQSFIATSTESGMRLLTVM  
HADKADKDKYARFTATNSLLNYITNTYEPNLVLAKGAAYKGKEASVRDGKE  
QSVIAVAKNDLKVVQKKNITKQNQLKINFKKELTAPITKKENLGKAYYVDLN  
KVGKGYLIKEPSVHLVAKDSIERSFFLKVWWNHFVRYVNEKL\*

## Sequence description:

- A] Length: 1236 bp - 412 aa (full-length gene sequence possibly)  
B] A possible Shine-Dalgarno sequence precedes the putative 'TTG' start codon. (needs further cloning and sequencing to verify N-terminus)

ID-173

Clone 3-60b

ATGACGCTTCGAGAATTAACAATAGAAGAATTTAAAGAACATTCAGGAAA  
TTATGATTCACAATCATTTTTACAAACACCTGAGATGGCTAAACTTTTAGA  
AAAACGCGGCTATGATGTTAGGTATTTGGGATATCAAGTAGAAAATAAAC  
TAGAGATAATCAGTTTATCTTATATTATGCCAGTCACTGGTGGTTTTCAAAT  
GAAAATTGATTCAGGACCAGTTCATTCAAATTCTAAGTATCTAAAACAATT  
TTATAAAGCATTGCAAGGCTATGCCAAATCCAACGGTGTTCTAGAATTAAT  
AGTTGAGCCTTTTGATGATTACCAATTATTTACTAGTTCGGGAGTTCCTAGT  
AATCAGGGAAATGATAATCTGATTGAAGATTTTACCAGTTCAGGTTATCAC  
CATGATGGTTTAAACAACCTGGTTTTACTGGTAAATATTTATCTTGGCACTATG  
TTAAAAATTTAGAAGGTGTCACCTCTGAAACGTTACTATCTTCATTCTCTAA  
GACAGGACGAGCTTTGGTTAAGAAAGCAATGTCTTTTGGAATCAAGGTTT  
GCGTTCTTAAACGTGATGAGCTACATTTATTTAAAGAGATAACAACCTTCTA  
CGTCAAATAGACGTGATTATATGGATAAGTCCTTAGATTATTATCAAGATT  
TTTACGATAGCTTTGAAGGCAAGGCTGAATTTGTGATTGCCACTTTAAATT  
TTAGAGAATACGACCATAACTTGCAAATAAAAGCTGAAGCATTGGAAAAT  
AAGCTT

MTLRELTIEEFKEHSGNYDSQSFLQTPEMAKLLEKRGYDVRYLGYQVENKLEI  
ISLSYIMPVTGGFQMKIDSGPVHSNSKYLKQFYKALQGYAKSNGVLELIVEPF  
DDYQLFTSSGVPSNQGNLIEDFTSSGYHHDGLTTGFTGKYLSWHYVKNLE  
GVTSETLLSSFSTGRALVKKAMSFGIKVRVLKRDELHLFKEITTSTSNRRDY  
MDKSLDYYQDFYDSFEGKAEFVIATLNFREYDHNLQIKAEALENKL

## Sequence description

- A) Length: 771 bp - 257 aa (partial gene sequence)  
B) This gene sequence was not identified using the LEEP system. It was identified immediately downstream of the ID-65 gene which was identified by

LEEP, during cloning and sequence analysis of the full-length ID-65 gene sequence. Sequence Characteristics:  
No obvious leader peptide sequence  
Orf is preceded by a potential Shine-Dalgarno sequence.

ID-174

Clone 2-17b (ID-80b)

TTGTCATTAAGTTTGGTTGCAGTGTTAAATCTTATCCCTCCTAAAATCATGG  
GATCAGTTATTGATGCTATTACAACCTGGAAAATTAACAAGACCACAATTAC  
TATGGAATTTATTAGGTTTGGTTTTGTCAGCTTTAGCTATGTATGGGCTGCG  
TTATATTTGGCGTATGTATATTTTAGGGACTTCTTACAAATTAGGCCAAGTT  
GTCAGATACCGTTTATTTGAACATTTTACAAAAATGTCTCCTTCTTTTTATC  
AGAAATATCGTACAGGTGATTTAATGGCGCACGCGACCAACGACATCAAT  
TCTCTAACACGTCTTGCAGGAGGAGGAGTTATGTCAGCAGTGGATGCCTCT  
ATCACAGCATTAGTAACGCTTATCACCATGTTCTTTACTATTTTCGTGGCAA  
ATGACATTAATTGCGGTTATCCCTTTGCCCTTAATGGCCTTAGCACTAGTA  
AATTGGGGCGAAAAACCCATGAAACCTTCAAAGAATCTCAGGCAGCCCTT  
TTCAGAATTAAATAATAAAGTG

MSLSLVAVLNLIPPKIMGSVIDAITTGKLTRPQLLWNLLGLVLSALAMYGLRYI  
WRMYILGTSYKLGQVVRYRLFHFETKMSPSFYQKYRTGDLMAHATNDINSLT  
RLAGGGVMSAVDASITALVTLITMFFTISWQMTLIAVIPLPLMALALVNWGEK  
PMKPSKNLRQPFSELNNKV

#### Sequence description

A) Length: 534 bp - 178 aa (partial gene sequence)

B) This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-80 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-80 gene sequence. Sequence Characteristics:

No obvious leader peptide sequence  
Orf is preceded by a potential Shine-Dalgarno sequence.

MHIETVIDFKELGKRYRFKNPTKELIADTLEQVLEVIKEVDYYQSQNYVVGYSY  
LSYEASAAFD SHFKVSQQLAGEHLAYFTVHKDCENEAFPLSYENVRLADNW  
TANVSEQEYQEAIANIKGQIRQGNTYQVNYTLELSQQLCSD

Sequence description:

A) Length: 440 bp - 146 aa (partial gene sequence)

B] This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-103 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-103 gene sequence. Shine Dalgarno sequence present upstream of ATG start codon, No apparent leader peptide sequence

ID-176

Clone 2-18/22b(b) (ID-104b)

GTGAATAATATGTTTTATCTCAAAATAGCCTGGCATAATTTAAAACATTCT  
ATAGACCAGTACATACCATTCTCTTAGCCAGTTTATTACTTTATTCATTGA  
CTTGTTCTACGCTACTAATCTTAATGAGTGCTGTTGGAAGAGATATGGGGA  
CAGCGGCAACGGTTCTTTTTCTTGGAGTGATTGTTTTGTCAATCTTTGCGGT  
AGTCATGGAACATTATAGCTACAATATCTTGATGAAACAGCGTAGTAGTG

AATTTGGACTGTATAACATTTTGGGGATGAATAAACGTCAAGTTGCGCGTG  
 TAGCTAGTCTAGAGCTGTTTATTATTTATATATTTCTTATTTCTATAGGAAG  
 TCTGTTTAGTGCTTTTTTTTGCTAAATTTATTTATTTAATTTTTGTCAACATTA  
 5 TTAACATCATGCACTAAATCTTAGTTTAAGTTTATGGCCATTTATTATTTG  
 TATCGTTATATTTACAGGTATTTTTCTGACTTTAGAAAGTTCCAGTTATTCGA  
 CATGTTCAATTTATCATCCCCATTAAGTCTTTTTAGAAAGAAACAACAGGGA  
 GAAAAAGAACCAAAAGGTAATCTTATACTTGCAATTTTAGCGTTAGTAGCT  
 ATCGCCATCGCTTATACAATGGCTCTTACTTCAGGTAAAGCACCTGCATTA  
 10 GCTGTTATCTATCGTTTCTTCTTTGCAGTACTTTTAGTAATTGCTGGTACTT  
 ATCTTTTTTATATTAGTTTTATGACATGGTACTTAAAAAGGTTGCGTCAAAA  
 CAAGCATTATTATTATAAATCTGAGCATTTTGTATCAACTTCGCAAATGAT  
 TTTTCGAATGAAGCAAAATGCAGTAGGGTTAGCAAGTATCACTTTATTAGC  
 TGTTATGGCTCTAGTTACTATTGCTACAACAGTCTCACTCTATTCAAATACA  
 CAAAATGTTGTTACCGGACTATTTCCAAAATCAGTAAGTTTATCAATAGAT  
 15 AATTCAAAAGGTGACGCGAAAAATATATTTGAAGAAAAGATTTTGAAGAA  
 ACTAGGTAAGTCATCTAAGGAAGCTATCACTTATAATCAGACAATGATTC  
 GATGCCAGTTAGTCAATCAAGTGACTTAATATCACATCTA  
  
 20 MNNMFYLKIAWHNLKHSIDQYIPFLLASLLLYSLTCSTLLILMSAVGRDMGTA  
 ATVLFLGVIVLSIFAVVMEHYSYNILMKQRSSEFGLYNILGMNKRQVARVASL  
 ELFIYIFLISIGSLFSAFFAKFIYLIFVNIINYHALNLSLSLWPFII CIVIFTGIFLTLE  
 25 VPVIRHVHLSSPLSLFRKKQQGEKEPKGNLILAILALVAIAIAYTMALTSGKAP  
 ALAVIYRFFFAVLLVIAGTYLFYISFMTWYLRRLRQNKHYYYKSEHFVSTSQM  
 IFRMKQNAVGLASITLLAVMALVTIATTVSLYSNTQNVVTGLFPKSVSLSIDNS  
 KGDAKNIFEEKILKKLGKSSKEAITYNQTMISMPVSQSDDLISHL  
  
 30

#### Sequence description:

- 35 A] Length: 1119 bp - 373 aa (partial gene sequence)  
 B] This gene sequence was not identified using the LEEP system. It was  
 identified upstream of the ID-104 gene which was identified by LEEP, during  
 cloning and sequence analysis of the full-length ID-104 gene sequence.  
 Possible Shine Dalgarno sequence present  
 40 upstream of a GTG start codon. Possesses a potential  
 leader peptide sequence

ID-177

Clone 2-5b (ID-112b)

5 ATGGTTGAGCCAATTATTTCAATACAAGGACTTCATAAAAAGTTTTGGGAAA  
AATGAGGTTTTTAAAAGGCATTGACTTGGATATTCATCAAGGAGAAGTGGT  
GGTTATTATTGGCCCTTCTGGCTCTGGTAAGTCAACATTTTTTAAGAACAAT  
GAATCTCTTGGAAGTACCAACAAAGGGAACAGTGACTTTTGAAGGGATTG  
ATATAACAGACAAAAAGAATGATATTTTTTAAAATGCGCGAAAAAATGGGC  
10 ATGGTTTTTCAACAGTTCAATCTATTTCCCAATATGACTGTACTAGAAAAT  
ATTACTTTATCACCTATTAAGACAAAGGGACTTTCTAAGCTTGATGCTCAG  
ACAAAAGCATACGAGCTACTTGAAAAAGTTGGACTCAAAGAGAAGGCTAA  
TGCTTATCCAGCAAGCTTATCTGGAGGACAACAACAACGGATTGCTATTGC  
AAGAGGTCTTGCAATGAATCCTGATGTCCTTCTTTTTGATGAACCTACTTCA  
15 GCTCTTGATCCTGAAATGGTAGGTGAAGTCTTGACTGTTATGCAAGATTTA  
GCTAAATCTGGTATGACGATGGTTATTGTCACTCATGAAATGGGTTTTGCA  
CGTGAAGTAGCGGATCGTGTCAATTATTATGGATGCAGGGATTATTGTTGAG  
CAAGGGACCCCTAAGAAAGTATTTGAGCAGACAAAAGAAATCCGCACAAG  
AGACTTCTTAAGTAAAGTATTATAA

25 MVEPIISIQGLHKSFGKNEVLKGDLDIHQGEVVVIIGPSGSGKSTFLRTMNLLE  
VPTKGTVTFEGIDITDKKNDIFKMREKMGMVFQQFNLFPNMTVLENITLSPIKT  
KGLSKLDAQTKAYELLEKVGLEKANAYPASLSGGQQQRIAIARGLAMNPDV  
LLFDEPTSALDPEMVGEVLTVMQDLAKSGMTMVIVTHEMGFAREVADRVIF  
MDAGIIVEQGTPKKVFQOTKEIRTRDFLSKVL\*

30      Sequence description:

- 35 A] Length: 735 bp - 244 aa (full length gene)  
B] This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-112 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-112 gene sequence. Shine-Dalgarno sequence precedes the 'ATG' start codon. No obvious leader peptide

40 ID-178

Clone 2-5c (ID-112c)



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5 ATGTTCTTGCAGGTCCTTGATGACGGTCGATTAAACAGATGGACAAGGAAG  
AACTGTTAGTTTTAAAGATACCATTATCATCATGACCTCAAATGCTGGTTC  
TGGTAAACTGAAGCAAGTGTTGGCTTTGGTGCCTCACGAGAAGGTAGGA  
CGAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGTCGACCTGCAGGCAT  
GCAAGC

10 MQPVKVDEPSVEETITILKGIQKKYEDYHHVKYNNDAIEAAAVLSNRYIQDRF  
LPDKAIDLLDEAGSKMNLTLNFVDPKEIDQRLIEAENLKAQATREEDYERAAY  
FRDQIAKYKEMQQQKVDDQDTPITEKTIEHIIIEKTNIPVGDLEKEQSQLINL  
ADDLKQHVIGQDDAVIKIAKAIRNRVGLGSPNRPIGSFLFVGPTGVGKTELSK  
QLAIELFGSADSMIRFDMSEYMEKHAVAKLVGAPPGYVGYEEAGQLTEKVRR  
NPYSLILLDEIEKAHPDVMHMFLLQVLDDGRLTDGQGRTVSFKDTIIMTSNAGS  
GKTEASVGFGASREGRTNSSSVPGDPLESTCRHAS

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Sequence description:

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A] Length: 1070 bp ÿ 356 aa (Partial gene sequence)

B] This gene sequence was not identified using the LEEP system. It was  
identified upstream of the ID-112 gene which was identified by LEEP, during  
cloning and sequence analysis of the full-length ID-112 gene sequence. Shine-  
Dalgarno sequence preceded the 'ATG'  
start codon. No obvious potential leader peptide  
sequence.

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ID-180

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Clone 2-7b (ID-113b)

35 ATGAGAGGGAAGGTTATTTACGGCACAACCCTTATAGGTCTTTTTCTATTC  
TTATTTTTCTATTTTTGGATTCCCTAAGCATCACATCGAGAGAATACATCATC  
ATCGTATAAAGCAGGTAGATGCGAAGAGTGATTTAACAGGATTTAAAACC  
CATTTGCCCATTCAGCATTGATACAAAGCAACAAGTTATTCCTCTTGTT  
ACAAAAGAAGGCGGAAAATATGTCAAAGCTAGGGATAATATTAATGTTGA  
TATCGAATTACGGGATTCTCCAAGTAGATCACATCATTTATCAGAAAAGCC  
40 GAGAATTAGGACAAAAGGGTTAATATCATATAGAGGAAATTCCTCTCGTT  
ACTTTGATAAGAAGTCATTGAAAGTTAAGTTTGTTACTAATAAGTTAAAGG  
AAAAGAAGCATCGATTAGCAGGAATGCCTAAAGAATCGGAGTGGGTATTG  
CATGGTCCCTTTCTAGACAGAACATTATTAAGAAATTATCTGAGTTATAAT

ATTGCTGGTGAGATTATGCCTATGCCCCAAACGTTTCGCTACTGTGAGTTAT  
TTGTCAATGGTGAGTATCAGGGAG

5 MRGKVIYGTTLIGLFLFLFFYFWIPKHHIERIHHHRIKQVDAKSDLTGFKTHLP  
SIDTKQQVIPLVTKEGGKYVKARDNINVDIELRDSPSRSHHLSEKPRIRTKGLIS  
YRGNSSRYFDKKSLSKVKFVTNKLKEKKHRLAGMPKESEWVLHGPFLLDRTLLR  
NYLSYNIAGEIMPMPQTFATVSYLSMVSIRE

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Sequence description:

A] Length: 582 bp - 194 aa (Partial gene sequence)  
B] This gene sequence was not identified using the LEEP system. It was  
15 identified downstream of the ID-113 gene which was identified by LEEP,  
during cloning and sequence analysis of the full-length ID-113 gene sequence.  
ATG start codon is preceded by a Shine-  
Dalgarno sequence-Possesses a potential leader peptide  
sequence. C-terminus to be determined.

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ID-181

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Clone 2-17b (ID-117b)

30 CTTACATTTTATTGATCACTATCTGACAAATGTTAATCAAACAGCAGTTCT  
TATTTTAGTGGGATATTATTCAATGTATGTCTTGCAGACCTTAATTCAATAT  
TTTGGGAATCTCTTTTTTGC GCGTGTCTTATAGTATTGTTAGAGATATTC  
GTAGAGATGCTTTTGCTAATATGGAAAGGCTAGGCATGTCTTATTTTGATA  
GGACACCGGCAGGATCTATTGTGTACGTATTACTAATGATACTGAAGCAA  
TATCTGATATGTTTTCGGGTATTTTATCAAGTTTTATCTCGGCGATATTTAT  
35 TTTTACAGTTACTCTGTACACTATGTTGATGCTAGACATTAACTAACAGG  
ACTCGTCGCTCTTTTGTTACCTGTTATCTTTATATTAGTGAATGTCTATCGG  
AAAAAATCAGTCACTGTCATTGCTAAAACGAGAAGTTTACTTAGTGATATC  
AACAGTAAATTATCAGAAAGTATTGAAGGAATTC

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SHFIDHYLTNVNQTA VLILVGYYS MYVLQTLIQYFGNLFFARVSYSIVRDIRRD  
AFANMERLGMSYFDRTPAGSIVSRITNDTEAISDMFSGILSSFISAIFFTVTLTYT  
MLMLDIKLTGLVALLLPVIFILVN VYRKKS VTVIKTRSLSDINSKLSE SIEGI

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B] This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-117 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-117 gene sequence. N- and C-termini have yet to be determined

ID-182

Clone 3-8b (ID-120b)

ATGTACCATATTGAATTAATAAAAGGAAGCTTTACTACCAAGAGAACGCCT  
AGTTGATTTAGGCGCAGATAGATTGAGTAATCAGGAGTTATTAGCCATTCT  
CTTACGTACAGGTATTAAGAAGAAAACCTGTTCTTGAAATTTCAACGCAAAT  
TTTAGAAAACATAAGCAGTTTAGCAGATTTTGGTCAATTATCCTTACAGGA  
GTTGCAATCCATTAAAGGAATCGGTCAGGTTAAATCCGTCGAAATAAAG  
CTATGCTAGAACTAGCAAAACGGATTACAAAGCTGAATATGATCGTAAA  
GAGCAAATTTTAAGTAGTGAACAATTAGCGAGGAAAATGATGCTCGAATT  
AGGGGATAAAAAACAAGAACATTTAGTAGCTATTTATATGGATACACAAA  
ATCGTATTATCGAACAGAGAACTATTTTTATTGGTACTGTACGTCGTTTACG  
TAGCAGAGCCAAGAGAAATTCTACATTATGCTTGTA AAAACATGGCAACT  
TCTTTGATTATTATACATAATCATCCCTCAGGTTCTCCAAATCCCAGTGAAA  
GTGATTTAAGTTTCACTAAAAAAATAAAACGATCATGTGATCATCTGGGAA  
TTGTCTGCCTAGATCACATCATCGTTGGAAAAAATAAATATTATAGTTTTT  
GAGAAGAAGCAGATATTTTATAA

MYHIELKKEALLPRERLVDLGADRLSNQELLAILLRTGIKEKPVLEISTQILENI  
SSLADFGQLSLQELQSIKGIGQVKSVEIKAMLELAKRIHKA EYDRKEQILSSEQ  
LARKMMLELGDKKQEHLVAIYMDTQNRHIEQRTIFIGTVRRSVAEPREILHYAC  
KNMATSLIIHNHPSGSPNPSESDLSFTKKIKRSCDHLGIVCLDHIIVGKNKYYSF  
REEDIL\*

Sequence description:

B] This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-120 gene which was identified by LEEP.

during cloning and sequence analysis of the full-length ID-120 gene sequence.  
ATG start codon is preceded by an typical  
Shine-Dalgarno sequence. No obvious leader  
peptide sequence

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ID-183

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Clone 3-11b (ID-121b)

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TGGTTAAAAGTAGTGATAGCTTGTATTCCATCTATTTTAATTGCTTTACCAT  
TTGATAATTGGTTTGAAGCTCATTTTAATTTTCATGATTCCGATTGCAATAGC  
CCTAATCTTTTATGGTTTTGTCTTCATATGGGTTGAAAAACGTAATGCACAC  
CTCAAACACAGGTAACCGAATTGGCAAGTATGTCCTTACAAGACAGCTTTC  
TTGATTGGATGTTTCCAGGTTCTCAGTATTGTTCCGGGAACCAGTCGTTCTG  
GAGCTACTATTTTAGGAGCAATTATTATTGGAAGTCTGTCGTTCCGGTCGCTG  
20 CTGACTTTACTTTCTTCCTTGCCATCCCAACTATGTTTGGTTATAGTGGACT  
TAAGGCGGTAAATATTTTTTAGATGGTAACGTCTTGAGTTTAGACCAATC  
TTTAATACTTTTAGTAGCAAGTCTGACAGCTTTCGTAGTTAGTTTATATGTT  
ATTCGTTTCTTGACAGACTATGTCAAACGACACGATTTCAACATCTTTGGT  
AAGTATCGTATAGTCTTAGGAAGTTACTCATCCTCTACTGGTTAGTTGTTC  
25 ATTTATTCTAA

30

WLKVVIACIPSILIALPFDNWFEAHFNFMIPAIALIFYGFVFIWVEKRNAHLKP  
QVTELASMSYKTAFLIGCFQVLSIVPGTSRSGATILGAIIGTSRSVAADFTFFLA  
IPTMFGYSGLKAVKYFLDGNVLSLDQSLILLVASLTAFVVSPLYVIRFLTDYVKR  
HDFTIFGKYRIVLGSLILYLWLVVHLF\*

Sequence description:

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A] Length: 579 bp - 193 aa (partial sequence)  
B] This gene sequence was not identified using the LEEP system. It was  
identified downstream of the ID-68 gene which was identified by LEEP,  
during cloning and sequence analysis of the full-length ID-68 gene sequence  
described in WO 00/06736. N-terminus has yet to be determined.

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ID-184

Clone 3-11c (ID-121c)

ATGGAAATGAAACAAATCAGTGAAACAACACTGAAAATTACAATTAGTAT  
5 GGAAGATTTAGAAGATCGTGGTATGGAGCTGAAAGATTCCTAATCCCTCA  
GGAGAAGACTGAGGAATTTTTCTATTCTGTCATGGATGAATTAGACTTGCC  
AGAAAACTTTAAAAATAGTGGTATGTTAAGTTTTTCGAGTAACACCTAAAA  
AAGATCGCATTGATGTTTTTGTACAAAGTCTGAATTAAGTAAAGATTTAA  
ATTTAGAAGAATTAGCAGATTTGGGTGACATTTCAAAAATGTCTCCAGAAG  
10 ACTTTTTTAAAACCTTGGAACAATCGATGTTGGAAAAAGGGGATACGGAT  
GCCCATGCCAAATTAGCAGAAATTGAAAATATGATGGATAAAGCAACTCA  
AGAAGTAGTTGAGGAAAATGTTTCTGAAGAACAACCTGAAAAGGAAGTAG  
AAACGATTGGATATGTTCACTATGTCTTTGATTTTGATAATATTGAAGCTGT  
AGTTCGATTTTCACAAACGATTGATTTTCCAATAGAAGCTT  
15 MEMKQISETTLKITISMEDLEDRGMELKDFLIPQEKTEEFFYSVMDELDLPENF  
KNSGMLSFRVTPKKDRIDVFVTKSELSKDLNLEELADLGDISKMSPEDFFKTLE  
QSMLEKGD TDAHAKLAEIENMMDKATQEVVEENVSEEQPEKEVETIGYVHY  
VFDFDNIEAVVRFSQTIDFPIEA

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Sequence description:

A] Length: 547 bp - 182 aa (Partial sequence)  
B] This gene sequence was not identified using the LEEP system. It was  
25 identified downstream of the ID-68 gene which was identified by LEEP,  
during cloning and sequence analysis of the full-length ID-68 gene sequence.  
ATG start codon is preceded by an typical  
Shine-Dalgarno sequence. No obvious potential  
30 leader peptide  
sequence

35 ID-185

Clone 3-16b (ID-122b)

40 GGAAACCAACGGCCAGTACAATCGTCAAGGGTAGATTATCCTAAACGTAG  
TCGTGCCAAGATTGTAGAAGTTTATTTTAGACAAGCTTCTACTACTGATTA  
TTCTGGTGTTTACAAAGGTTACTATATTGACTTTGAAGCCAAAGAAACCCG  
GCAGAAAAC T GCTATGCCTATGAAAAATTTTCATGCTCACCAAATAGAGC  
ACATGGCAAATGTATTACAGCAAAAAGGGATTGCTTTGTCTTGCTTCATT

TTTCCACACTTAAGGAAACCTATCTACTCCCTGCTAATGAGTTAATTTTCATT  
TTATCAGATTGATAAAGGCAATAAATCAATGCCTATTGATTATATCAGAAA  
AAATGGATTTTTCGTAAAGGAGAGTGCCTTTCCTCAAGTCCCTTACTTAGA  
TATTATTGAAGAAAAATTATTAGGCGGTGATTACAATTAA

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GNQRPVQSSRVDYPKRSRAKIVEVYFRQASTTDYSGVYKGYIIDFEAKETRQ  
KTAMPMKNFHAHQIEHMANVLQQKGICFVLLHFSTLKETYLLPANELISFYQI  
DKGNKSMPIDYIRKNGFFVKESAFPQVPYLDIIEEKLLGGDYN\*

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Sequence description:

A] Length: 447 bp - 149 aa (partial sequence)

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B] This gene sequence was not identified using the LEEP system. It was  
identified upstream of the ID-122 gene which was identified by LEEP, during  
cloning and sequence analysis of the full-length ID-122 gene sequence. N-  
terminus has yet to be determined

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ID-186

Clone 3-17b (ID-123b)

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GGATCCTAAAAACGCTAAGGTTTATCAAAAAAATGCTGATCAATTTAGTG  
ACAAGGCAATGGCTATTGCAGAGAAGTATAAGCCAAAATTTAAAGCTGCA  
AAGTCTAAATACTTTGTGACTTCACATACAGCATTCTCATACTTAGCTAAG  
CGATACGGATTGACTCAGTTAGGTATTGCAGGTGTCTCAACCGAGCAAGA  
ACCTAGTGCTAAAAAATTAGCCGAAATTCAGGAGTTTGTGAAAACATATA  
AGGTTAAGACTATTTTGTGTTGAAGAAGGAGTCTCACCTAAATTAGCTCAAG  
CAGTAGCTTCAGCTACTCGAGTTAAAATTGCAAGTTTAAGTCCTTTAGAAG  
CAGTTCCCAAAAACAATAAAGATTACTTAGAAAATTTGGAAACTAATCTTA  
AGGTACTTGTCAAATCGTTAAATCAATAG

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35

DPKNAKVYQKNADQFSDKAMAIAEKYKPKFKAAKSKYFVTSHTAFSYLAKR  
YGLTQLGIAGVSTEQEPSAKKLAEIQEFVKTYKVKTIFVEEGVSPKLAQAVAS  
ATRVKIASLSPLEAVPKNNKDYLENLETNLKVLVKSLNQ\*

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Sequence description:

A] Length: 433 bp - 144 aa (partial sequence)

B] This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-123 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-123 gene sequence. N-terminus has yet to be determined

ID-187

Clone 3-46/47 (ID-130b)

ATGAAAAAAGTCATCGATT TAAAAAACTACAAAAAGCATACGCCTCAGA  
AACTGTTTTAAATAATATTAATTTGGAGGTGTTTAAAGGAGAAATAATTGG  
ATTAATAGGACCCTCTGGAGCAGGGAAATCTACCTTGATTAAAACTATGCT  
TGGCATGGAAAAAGCAGATAAGGGAACAGCTCTTGTTCTTGATACTCAA  
TGCCAGATCGTAATATTTTAAATCAAATTGGCTATATGGCTCAATCTGATG  
CCTTACACGAGTCTTTAACTGGCTTAGAAAATTTATTATTCTTTGGAAAA  
TGAAAGGTATTCAAAAAACTGAATTA AAAACAGCAGATAACTCATATTTCT  
AAAGTAGTAGATCTAGAAAACCAACTTGATAAATTTGTCTCAGGTTACTCA  
GAAGGTATGAAAAGACGGCTTCTCTAGCCATCGCCCTACTTGGAACCCC  
ACAGTTTTAATCCTAGATGAACCTACCGTTGGAATTGATCCATCCTTGAGG  
AGAAAAATCTGGCAAGAGCTAATTAATATTAAGGATGAAGGACGTTCTAT  
CTTTATTACAACCCACGTTATGGATGAAGCAGAATTAACAAGTAAGGTTGC  
ACTACTATTACGTGGAAACATTATTGCCTTTGATACTCCATTACATTTAAA  
AAAACAATTTAATGTGAGTACTATTGAGGAAGTTTTCTTAAAAGCTGAAGG  
AGAATAA  
MKKVIDLKKLQKAYASETVLNNINLEVFKGEIIGLIGPSGAGKSTLIKTMLGME  
KADKGTALVLD TQMPDRN ILNQIGYMAQSDALHESLTGLENLLFFGKMKGIQ  
KTELKQQITHISKVVDLENQLDKFVSGYSEG MKRRLSLAIAL LGNPTVLILDEP  
TVGIDPSLRRKIWQELINIKDEGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTP  
LHLKKQFNVSTIEEVFLKAEGE\*

Sequence description:

A] Length: 717 bp - 239 aa (Possible full-length sequence)

B] This gene sequence was not identified using the LEEP system. It was identified upstream of the ID-130 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-130 gene sequence. ATG start codon is preceded by a possible



Shine-Dalgarno. No obvious potential leader  
peptide sequence

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ID-188

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Clone 3-83b (ID-144b)

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ATGGTACAAATGATACATGATATGATTAAAACAATTGAGCATTTTGCTGAG  
ACACAAGCTGATTTTCCAGTGTATGATATTTTAGGGGAAGTCCATACTTAT  
GGACAACCTTAAAGTAGACTCTGACTCTCTAGCTGCTCATATTGATAGCCTA  
GGCCTTGTTGAAAAATCACCTGTCCTTAGTATTCGGTGGTCAAGAATATGAA  
ATGTTGGCGACATTTGTTGCTTTAACAAAGTCAGGGCATGCTTATATACCG  
GTTGACCAACACTCTGCTTTGGATAGAATACAGGCTATTATGACAGTTGCT  
CAACCAAGCCTTATCATTTC AATTGGTGAATTCCTCTTGAAGTTGATAAT  
GTCCCAATCCTAGACGTTTCTCAAGTTTCAGCTATTTTGAAGAAAAGACT  
CCTTATGAGGTAACACATTCTGTAAAGGTGATGATAATTACTATATTATT  
TTCACCTCAGGGACTACTGGTTTACCAAAAAGGTGTGCAAATTTACATGAC  
AATTTATTGAGCTTTACAAATTGGATGATTTCTGATGATGAGTTTTCAGTTC  
CTGAAAGACCGCAAATGTTGGCTCAACCC

25

MVQMIHDMIKTIEHFAETQADFPVYDILGEVHTYGQLKVDSDSLAAHIDSLGL  
VEKSPVLVFGGQEYEMLATFVALTKSGHAYIPVDQHSALDRIQAIMTVAQPSL  
IISIGEFPLEVDNVPILDVSQVSAIFEEKTPYEVTHSVKGDDNYIIFTSGTTGLP  
KGVQISHDNLLSFTNWMISDDEFSVPERPQMLAQP

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Sequence description:

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A] Length: 592 bp - 197 aa (partial sequence)  
B] This gene sequence was not identified using the LEEP system. It was  
identified downstream of the ID-144 gene which was identified by LEEP,  
during cloning and sequence analysis of the full-length ID-144 gene sequence.  
Putative ATG start codon is preceded by a  
typical Shine-Dalgarno sequence. No obvious  
leader peptide sequence  
This orf is not in frame with nuc

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ID-189

## Clone 3-86b (ID-145b)

5 ATGGAAAATCATCGTTATGAAGATGAAGGTAAATTCCAGCGTAAGATGAC  
CAGTCGTCATCTCTTTATGTTATCGCTAGGTGGTGTATCGGGACTGGGCTT  
TTCTTGAGTTCAGGTTATAACATTGCACAGGCTGGTCCGCTTGGAGCTGTG  
10 CTGTCTTATTTGATTGGTGCCGTTGTGGTTTATTTGGTCATGCTATCACTTG  
GGGAATTGGCGGTTGCCATGCCGGTGACGGGGTCATTCCACACTTATGCCA  
CTAAGTTTATCAGTCCTGGAACAGGTTTTACTGTTGCTTGGCTATATTGGAT  
TTGTTGGACGGTCGCCTTGGGGACTGAATTTTTAGGTGCTGCCATGCTGAT  
GCAGCGCTGGTTCCCAAATGTGCCGGCTTGGGCATTTGCTTCCTTTTTTGCC  
CTTGTGATTTTTGGTTTAAATGCTCTTAGCGTACGCTTTTTTGCAGAAGCAG  
15 AGTCTTCTCTCAAGTATTAAGGTTATTGCTATCATTATCTTTATTATCTTG  
GGCTTAGGTGCTATGTTTGGTCTAGTTTCCTTTGAAGGTCAGCACAAAGGCT  
ATTCTCTTCACTCATCTGACTGCCAATGGTGCCTTTCCAAATGGTATCGTTG  
CAGTTGTCTCAGTCATGTTGGCTGTAACTATGCCTTCTCTGGTACTGAGTT  
AATTGGTATTGCGGCTGGTGAAACGGATAATCCCAAAGAAGCTGTACCAA  
20 GGGCTATTAAAACGACAATCGGTCGCTTGGTTGTTTTCTTTGTACTGACAA  
TTGTTGTCCTAGCTTCGCTATTGCCAATGAAAGAGGCAGGCGTATCCACAG  
CACCATTTCGTTGATGTCTTTGACAAGATGGGAATCCCTTTTACGGCGGATA  
TCATGAACCTTCGTTATCTTGACAGCCATCCTGTCTGCTGGTAACTCAGGTCT  
CTACGCATCAAGCCGTATGCTCTGGTCCCTTGCCAATGAAGGTATGTTGTC  
25 AAAATCTGTTGTGAAAATCAATAAACACGGTGTCCCAATGCGTGCTCTTCT  
CTTGTCAATGGCAGGAGCAGTGCTGTGCGCTCTTTTCAAGTATTTACGCTGC  
AGACACAGTTTATCTAGCCTTGGTTTCAATCGCGGGCTTTGCTGTTGTTGTC  
GTATGGCTAGCCATTCCAGTCGCACAAATCAATTTCCGCAAGGAATTC

30 MENHRYEDEGKFQRKMTSRHLFMLS LGGVIGTGLFLSSGYTIAQAGPLGAVL  
SYLIGAVVVYLVMLSLGELAVAMPVTGSFHTYATKFISPGTGFTVAWLYWIC  
WTVALGTEFLGAAMLQMQRWFPNPVPAWAFASFFALVIFGLNLSVRFFAEAES  
FFSSIKVIAIIIFIILGLGAMFGLVSFEGQHKAILFTHLTANGAFPNGIVAVVSVM  
LAVNYAFSGTELIGIAAGETDNPKEAVPRAIKTTIGRLVVFFVLTIVVLASLLPM  
35 KEAGVSTAPFVDVFDKMGIPFTADIMNFVILTAILSAGNSGLYASSRMLWSLA  
NEGMLS SVVKINKHGVP MRALLLSMAGAVLSLFSSIIYAADTVYLALVSIAGF  
AVVVVWLAIPVAQINFRKEF

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Sequence description:

A] Length: 1126 bp - 393 aa (partial gene

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A] Length: 637 bp - 231 aa (partial sequence)

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ATGACTAATATCTCAGATGTTCCAAAAGCTATTAGAACACAGGCACAGTAT  
GTTCTCTTGGGAATGAGAGTTATGGATCAGTCGGTATTACCGAAAACATAT  
AATTCAAAAGAACCTTATTTGAAACCAGATATGATTTATATTCATGATAGA

AGACAAGAGACAATGCTTAAAATCACTCAAGAAATAGAAATGGAGCATTG  
A

MTNISDVPKAIRTQAQYVLLGMRVMDQSVLPKTYNSKEPYLKPDMIYIHDRR  
QETMLKITQEIEMEH\*

#### Sequence description

A] Length: 204 bp - 68 aa (partial sequence)

B] This gene sequence was not identified using the LEEP system. It was identified upstream of the ID-155 gene which was identified by LEEP, during cloning and sequence analysis of the ID-155 gene sequence.

ATG start codon is preceded by a potential typical Shine-Dalgarno sequence.

Has a

typical leader peptide. N-terminus has yet to be verified

ID-193

Clone 2-54altb (ID-172b)

AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCTGGGGGAATATAAATT  
TGGATTTTCATGACGATGTAAAGCCAATTTATTCTACGGGAAAAGGTCTAAA  
TGAGGCTGTTATTCGTGAGTTATCTGCAGCTAAGGGTGAACCTGAGTGGAT  
GTTGGACTTTCGTCTAAAATCCTTGGAACGTTTAATAAAATGCCGATGCA  
GACCTGGGGAGCAGATTTATCAGATATTGATTTTGATGATATTATTTATTA  
TCAAAAAGCATCTGATAAACCTGCGCGTGATTGGGATGATGTTCCAGAAA  
AAATCAAAGAACTTTTGAAAGAATTGGGATTCCAGAAGCTGAAAGAGCC  
TATCTTGCAGGAGCATCAGCACAATATGAATCAGAAGTAGTTTATCACAAT  
ATGAAAGAAGAATATGATAAGCTGGGTATTGTTTTTACGGATACTGACTCT  
GCACTTAAAGAGTACCCAGAGCTATTCAAAAAATATTTTGCTAAACTTGTC  
CCTCCAACAGATAATAAATTAGCTGCTCTGAACTCTGCTGTATGGTCAGGT  
GGAACATTTATTTATGTTCTAAAGGTGTAAAGGTGGATATTCCACTTCAA  
ACTTACTTCCGTATTAATAATGAAAATACTGGACAATTTGAACGTACTCTC  
ATTATTGTTGATGAGGGAGCAAGTGTTCACTATGTTGAAGGTTGTACCGCC  
CCAACCTATTCTTCAAATAGTTTACATGCAGCTATAGTTGAAATTTTTGCAC  
TTGATGGAGCTTATATGCGCTATACGACTATTCAAAATTTGGTCCGATAATG  
TCTATAATTTAGTGACAAAACGTGCTACCGCTAAAAAAGATGCAACAGTT  
GAGTGGATAGATGGAAATCTAGGAGCTAAAACAACAATGAAATACCCATC

GGTTTACCTTGATGGTGAAGGAGCACGTGGCACGATGTTGTCTATTGCTTT  
TGCAAACAAAGGACAACACCAAGATACGGGTGCAAAGATGATTCATAATG  
CCCCCATACTAGTTCATCCATTGTCTCTAAATCAATTGCTAAGGGTGGGG  
GAAAAGTTGATTATCGAGGTCAAGTGACATTTAATAAAGATTCCAAAAA  
5 TCAGTGTACATATAGAATGTGACACCATATTGATGGATGATATTTCAAAA  
TCAGATAACCATAACCGTTTAATGAGATTTCATAATTCACAGGTTGCTTTAGAG  
CATGAAGCAAAGGTGTCTAAGATTTCTGAAGAGCAACTGTACTACTTGATG  
AGTCGAGGTTTATCTGAAGCTGAAGCAACAGAAATGATTGTTATGGGGTTT  
GTTGAGCCCTTTACGAAAGAATTACCAATGGAATATGCGGTAGAGTTAAA  
10 TCGTTTAATTCCTATGAAATGGAAGGTTTCAGTTGGTTAA

MHACRSTLEDLGEYKFGFHDDVKPIYSTGKGLNEAVIRELSAAKGEPEWMLD  
FRLKSLETFNKMPMQTWGADLSDIDFDDIYYQKASDKPARDWDDVPEKIKE  
15 TFERIGIPEAERAYLAGASAQYESEVVYHNMKEEYDKLGIVFTDSDSALKEYP  
ELFKKYFAKLVPPTDNKLAALNSAVWSGGTFIYVPKGVKVDIPLQTYFRINNE  
NTGQFERTLIIVDEGASVHYVEGCTAPTYSSNSLHAAIVEIFALDGAYMRYTTI  
QNWSDNVYNLVTKRATAKKDATVEWIDGNLGAKTTMKYPSVYLDGEGARG  
TMLSIAFANKGQHQDTGAKMIHNAPHTSSSIVSKSIAGGGKVDYRGQVTFN  
20 KDSKKSVSHECDTILMDDISKSDTIPFNEIHNSQVALEHEAKVSKISEEQLYYL  
MSRGLSEAEATEMIVMGFVEPFTKELPMEYAVELNRLISYEMEGSVG\*

Sequence description:  
25

A] Length: 1411 bp - 469 aa (Possible full-length gene)  
B] This gene sequence was not identified using the LEEP system. It was  
identified downstream of the ID-72 gene which was identified by LEEP,  
during cloning and sequence analysis of the full-length ID-72 gene sequence.  
30 No obvious Shine Dalgarno sequence upstream of  
TTG start codon (insufficient sequence data). N  
terminus needs verification.

35

ID-194

Clone 3-1b (ID-81b)

40 ATGATAGAATTCTTTTCTAATATCAGAACAGAGATTCCGCAGATGCCTTTA  
CTTATCCATAGTTTGATTTTATCTGTCTTACCTTTTCTGATGTGGCTGACTTT  
GGTTAATAGAGATAAGCCTTTGTATAAACTATTTGGAGTATCCTTTTAGG  
ACTTCAGTTAATTACGATTTATACTTGGTTTTTCTGGGCAAAATTGCCTTTA

TCTGAAAGTCTTCCCCTTTACCATTGTCTGAATAGGCATGTTTGTCTGGTCTCT  
TA

5 MIEFFSNIRTEIPQMPLLIHSLILSVLPFLMWLTLVNRDKPLYKTIWSILLGLQLI  
TIYTWFFWAKLPLSESLPLYHCRIGMFVGLL

Sequence description

- 10 A) Length: 261 bp - 87 aa (partial gene sequence)  
B) This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-81 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-81 gene sequence. Sequence Characteristics: Possesses a potential leader peptide sequence. Orf is preceded by a potential Shine-Dalgarno sequence.

15

ID-195

20

Clone RS-55b

25 AAGCTTGTGCAAAGTATTAAAGAGATAGGATTAGCTAATGCGCATTTATTA  
GCTGTTGCTCCGACAGGGTCAATCAGTTATCTTTCTTCTTGTACTCCGAGCC  
TTCAACCGGTTGTATCACCTGTCTGAAGTACGCAAGGAAGGAGCACTGGGG  
AGGGTTTATGTAGCTGCTTATAAGATTGATGCAGATAATTATGTCTACTAC  
AAAAAAGGAGCTTATGAAGTGGGATCTGAGGCGATTATCAATATTGCAGC  
TGCCGCTCAAAAACACATTGATCAAGCTATTTTCGTTAACGCTTTTCATGAC  
30 AGATCAAGCAACTACGCGAGATTTAAATAAAGCCTATATTCAAGCATTTA  
AACAAAAATGTGCCTCTATTTATTATGTACGAGTGAGACAGGACATCCTAG  
AAGGTAGCGAGAGTTATGATGATATGCTGGATGATTTCACTTCATCGGACT  
TAGAAGACTGTCAATCCTGCATGATTTAA

35

>KLVQSIKEIGLANAHLAVAPTGSISYLSSCTPSLQPVVSPVEVRKEGALGRV  
YVAAYKIDADNYVYYKKGAYEVGSEAIIINIAAAQKHIDQAISLTLFMTDQAT  
TRDLNKAYIQAFKQKCASIYYVRVRQDILEGSESYDDMLDDFTSSDLEDCQSC  
MI\*

40

Sequence description:

A] Length 486 bp - 162 aa (Partial sequence)

B] This gene sequence was not identified using the LEEP system. It was identified upstream of the ID-87 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-87 gene sequence. N-terminus to be determined.

ID-196

Clone RS-59(ID-90b)

GTGAGGACATATATTACAAACTTGAATGGACATTCAATCACTAGTACAGC  
ACAAATAGCTCAAAACATGGTAACAGATATAGCAGTAAGCTTAGGTTTTC  
GTGAGCTGGGAATACATTCTTATCCGATTGATACTGATTCTCCTGAGGAAA  
TGAGTAAGCGTTTAGATGGAATCTGTTCCGGACTTAGAAAAAATGATATTG  
TCATATTTTCAGACACCTACATGGAACACTACAACCTTTTGATGAAAAATTAT  
TTCACAAATTAAAAATATTTGGTGTAAGATTGTTATTTTTATACATGATGT  
TGTACCGCTAATGTTTGATGGAAATTTTATTTGATGGATAGAAGTATAGC  
TTATTATAATGAAGCAGATGTTTAATAGCCCCTAGTCAAGCAATGGTTCGAT  
AAGCTT

MRTYITNLNGHSITSTAQIAQNMVTDIAVSLGFRELGIHSYPIDTDSPEEMSKRL  
DGICSGLRKNDIVIFQTPTWNTTTFDEKLFHKLKIFGVKIVIFIHDVVPLMFDGN  
FYLMDRTIAYYNEADVLIAPSQAMVDKL

Sequence description:

A] Length: 414 bp - 138 aa(partial gene)

B] This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-90 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-90 gene sequence.

No obvious signal peptide, but a possible Shine Dalgarno sequence is present upstream of ATG start codon. C-terminus has yet to be determined.

ID-197

Clone RS-59c (ID-90c)



5 CATGGAAATGAAGTTGATGATGTTATTAGAAGGGCATTGGAATATAATCAC  
CTTATCTTTGCTTTTGATAATACTGTGCATAACAGAGAGTTAGTATTAGATA  
GCAATATCATTCTCACACAACCTGTGAACAATTGATAAATTTAATGAAAA  
ATTTATCAGGCTCCATTATGTATTTGCTAGAGCAACAAAGAGAACAAACA  
AGTAATGAAACAAAAGAGCGTTATAAAGAAATATTAGGAGGGTATGGAA  
ATGCCTAA

10 HGNEVDDVIRRAFEYNHLIFAFDNTCHNRELVLDSNIISHTTCEQLINLMKNLS  
GSIMYLLEQQREQTSNETKERYKEILGGYGNA\*

15 Sequence description:

A] Length: 261 bp - 87 aa(partial gene sequence)

20 B] This gene sequence was not identified using the LEEP system. It was  
identified upstream of the ID-90 gene which was identified by LEEP, during  
cloning and sequence analysis of the full-length ID-90 gene sequence. N-  
terminus has yet to be determined

25 ID-198

Clone RS-70b (ID-93b)

30 ACATTTTTATATTATGTATTTGAAGACGTAGCCACCCAGTCAAATATGACT  
GGGAAGATTTTTAGTATGTCTAAAGAAGAGTTGTCATATTTACCCGTTATT  
AAACTTTTTAAGAATCAAGGTGTATACAACGGCTTGATTGGTCTATTCCTC  
CTTTATGGGTATATATTTACACAGAATCAAGAAATTGTAGCTATTTTTTTAA  
TCAATGTGTTGCTAGTTGCTGTTTATGGTGCTTTGACAGTTGATAAAAAAA  
35 TCTTATTAACAGGGTGGTTTACCTATATTAGCTCTTTTAACATTCTTATT  
TTAA

TFLYYVFEDVATQSNMTGKIFSMSKEELSYLPVIKLFKNQGVYNGLIGLFLLY  
GLYISQNQEIVAIFLINVLLVAVYGALTVDKKILLKQGGLPILALLTFLF\*

40

Sequence description:

A] Length: 312 bp - 104 aa (partial gene sequence)

B] This gene sequence was not identified using the LEEP system. It was identified upstream of the ID-93 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-93 gene sequence.

5 N-terminus has yet to be determined

ID-199

10 Clone RS-70c (ID-93c)

ATGAAATTAAGTGTCTTGATTATGGGCTTATTGATTATGGAAAACTGCA  
AGTGATGCAATACAAGAAACGATTCTTTTATCACAAGAGGCGGAGCAACT  
AGGCTATCATCAATTTTGGGTGGCTGAACATCACGGTGTTAAGGCATTTCAG  
15 TATTAGCAATCCAGAATTAATGATAATGCATTTGGCTAACCAGACTAAATC  
TATCAAAATTGGCTCTGGAGGTATAATGCCTCTGCACTATAGTAGTTTTAA  
ACTCGCGGAGACTCTCAAGACATTAGAGACATGTCATCCGAATCGAGTAA  
GTATTGGTTTATAGGAAATTCAGTGGGACAGTTAAAGTTTCAAATGCACTTC  
GTAGCTTACATAAAGCACATGATTACGAAGAGGTACTGGAGGAATTGAAG  
20 TCATGGCTTATTGATGAATCATCCAGTAAGGAACCATTAGTTCAACCGACT  
CTTTCTAGCTTCCCAGACTTATATGTGTTGGGGAGTGGTCAAAAATCAGCT  
TATTTAGCGGCTAACTTGGCTTAGGCTTACCTTCGGTGTTCCTTTTA  
TGGACAAAGACCCATTGACAGAAGCTAAA

25 MKLSVLDYGLIDYGKTASDAIQETILLSQEAEQLGYHQFWVAEHHGVKAFFSIS  
NPELMIMHLANQTKSIKIGSGGIMPLHYSSFKLAETLKTLETCHPNRVSIGLGN  
SLGTVKVSNALRSLHKAHDYEEVLEELKSWLIDESSSKEPLVQPTLSSFPDLYV  
LGSGQKSAYLAACLGLGFTFGVFPFMDKDPLTEAK

30 Sequence description:

A] Length: 588 bp - 196 aa (partial)

35 B] This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-93 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-93 gene sequence. No obvious signal peptide, but Shine Dalgarno sequence upstream of the ATG start codon.